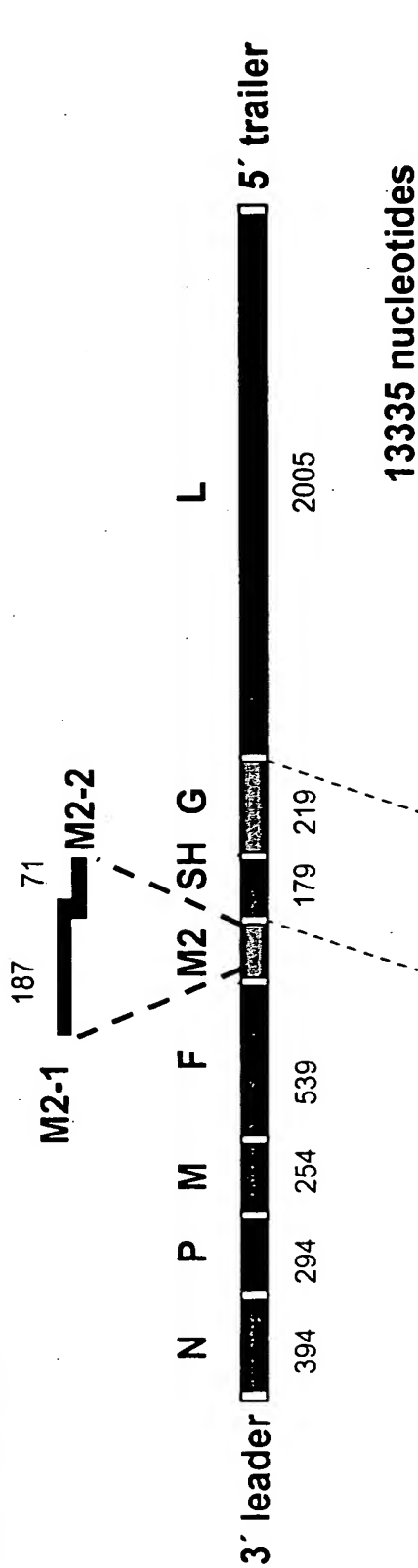


# HMPV 83



# RSV A2

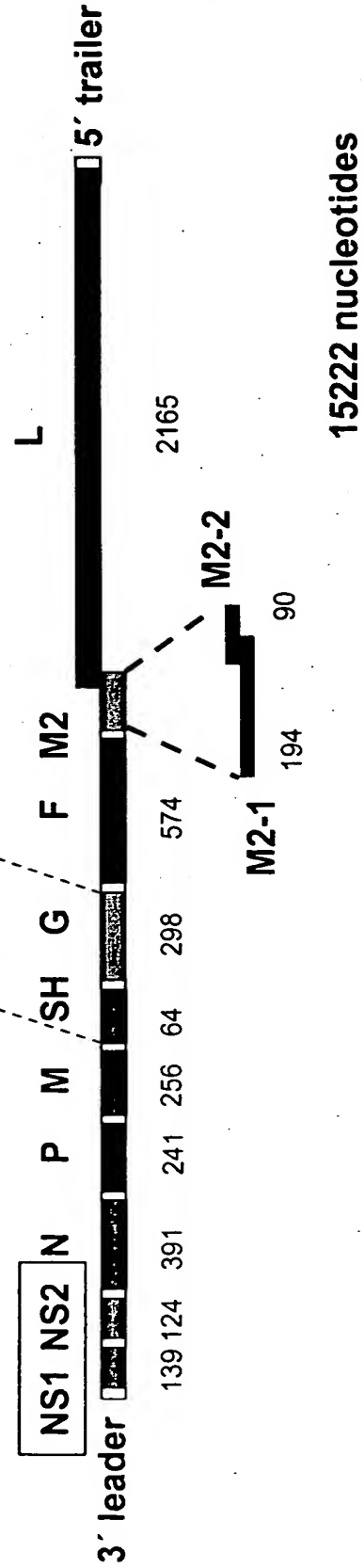
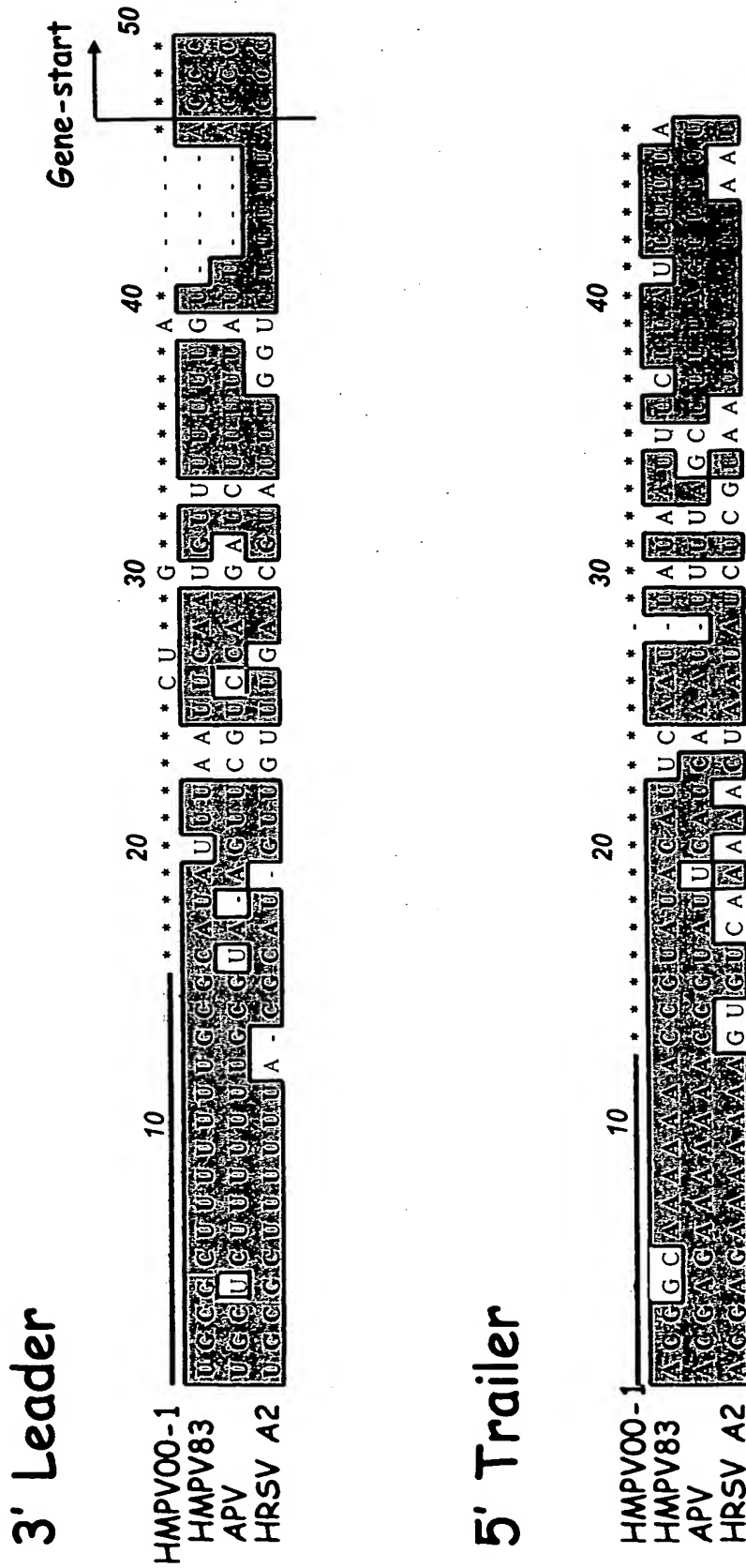


Fig. 1



— Sequences previously unknown for any human metapneumovirus

Fig. 2

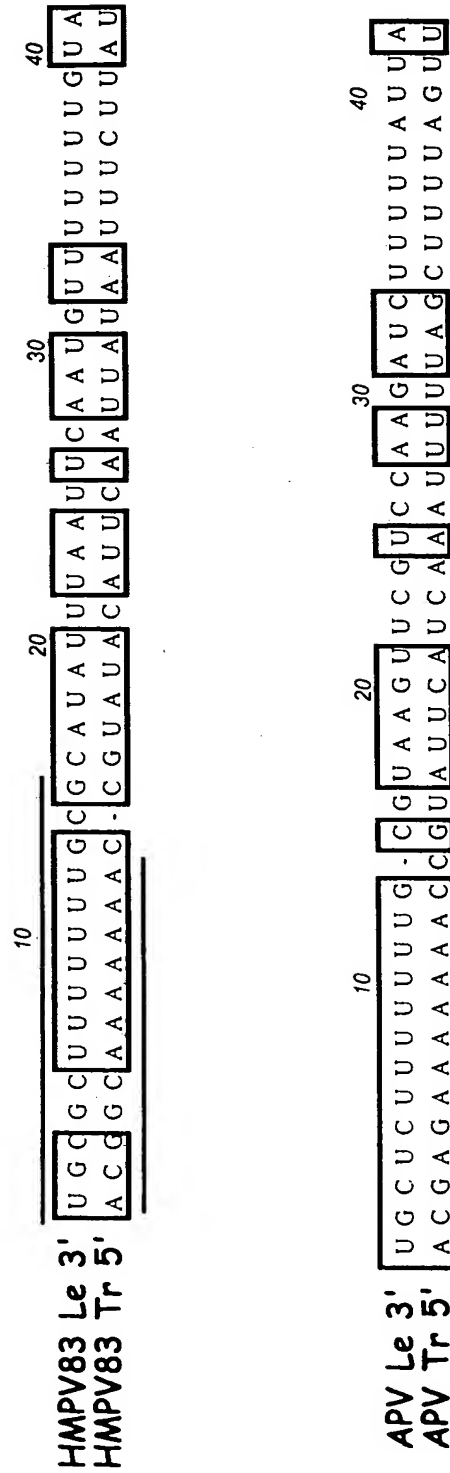


Fig. 3

# Examples of differences between HMPV 83 and HMPV 00-1

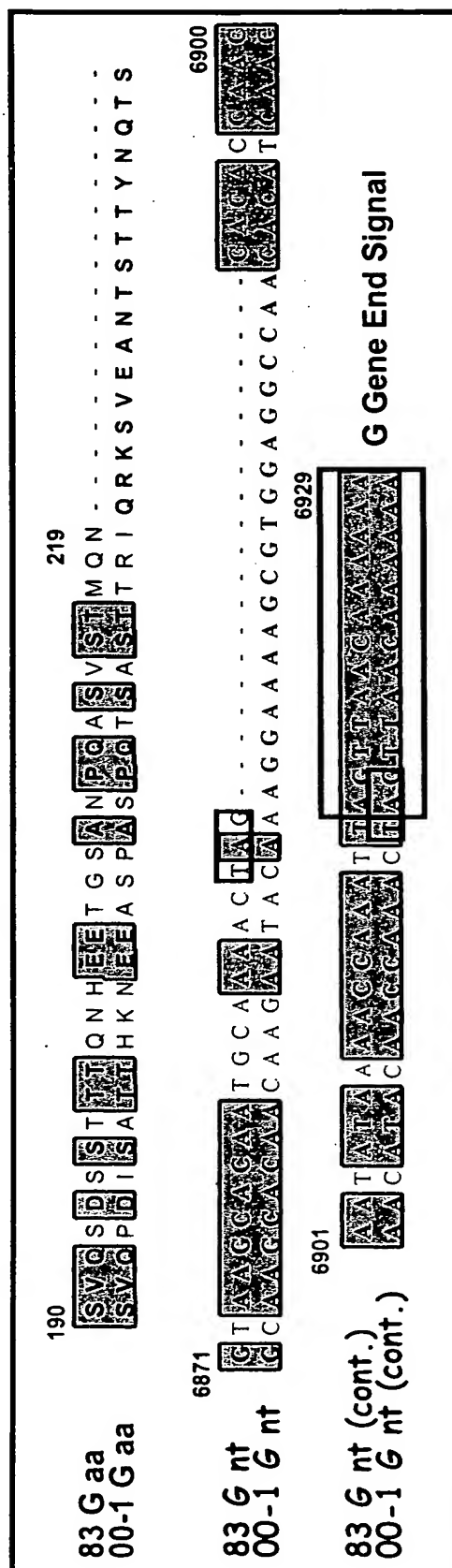


Fig. 4

# Amino acid identity between HMPV83 and other Pneumoviruses for the indicated proteins

	N	P	M	F	M 2-1	M 2-2	G	SH	L
HMPV 00-1	99	95	99	98	98	96	70	85	99
HMPV 97-82	95	85	97	94	ND	ND	ND	ND	ND
APV A	70	58	77	68	73	25	12	20	64
APV B	69	53	76	67	71	27	ND	20	ND
APV C	88	68	87	81	83	56	ND	ND	ND
HRSV A2	41	31	38	36	36	12	15	6	46
HRSV B	41	31	37	35	35	8	15	6	46
BRSV	41	31	37	37	35	14	19	10	46
PVM	45	28	38	40	36	12	ND	8	ND

ND: Comparison not done, usually because sequence was unavailable

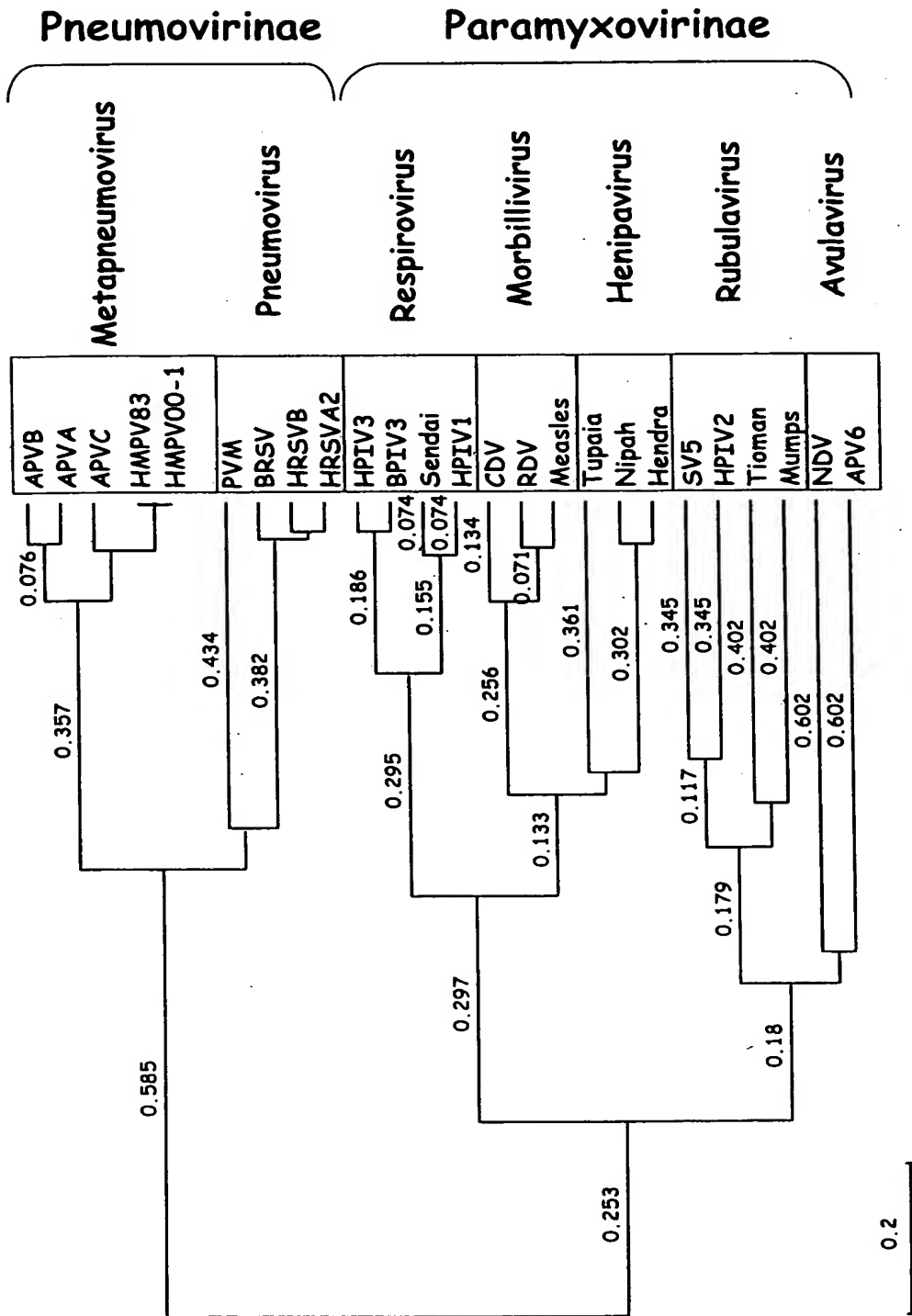


Fig. 6

# HMPV 83 13335 bases

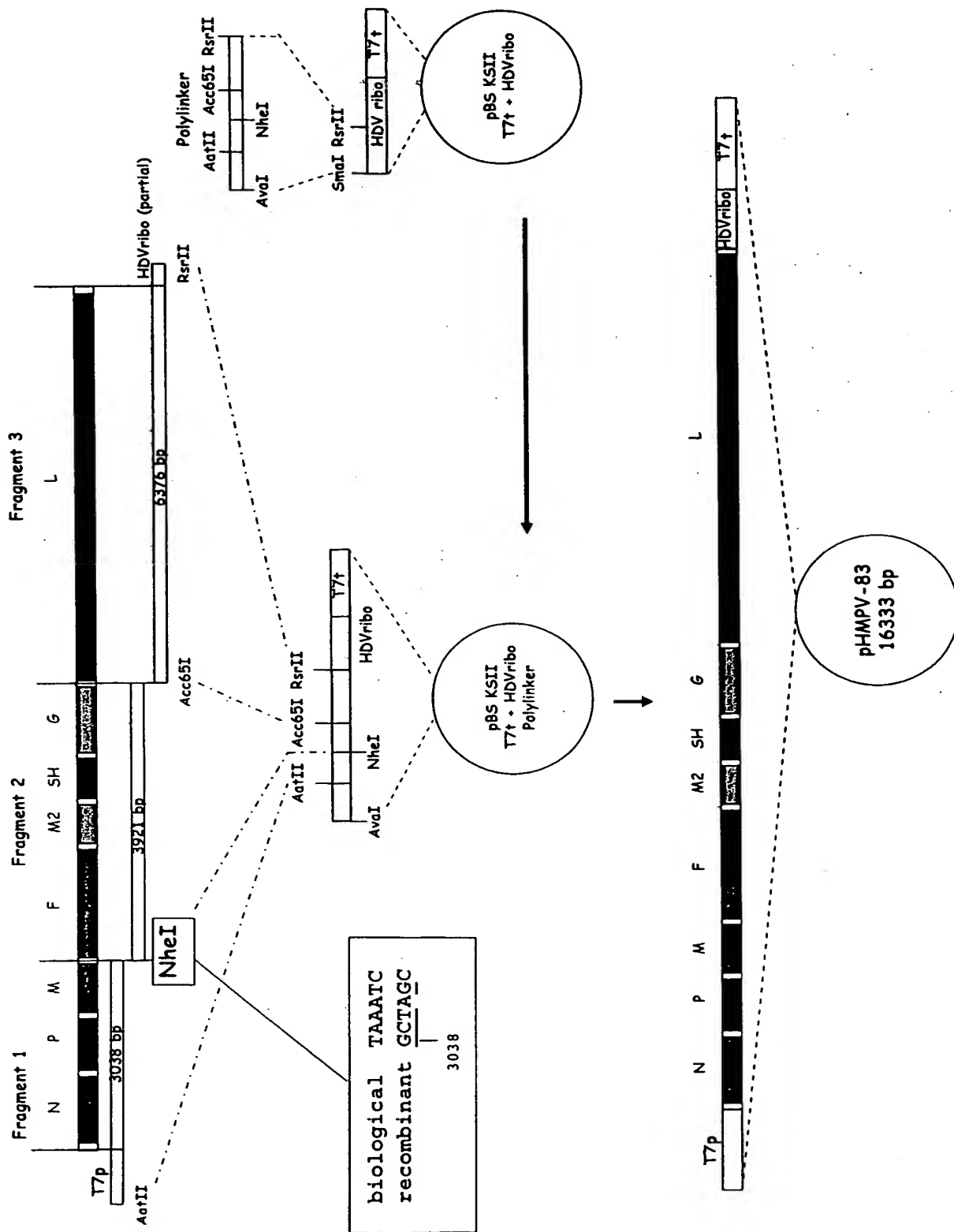


Fig. 7

# Gene Start Signal

	1	5	10	15
N	tacaaaaaacat	GGGACAAAGTGAAA	ATGtctcttc	
P	taattaaaaaagt	GGGACAAAGTCAAA	ATGtcatctcc	
M	aaaaataaaaaat	GGGACAAAGTGAAA	ATGgagtcct	
F	atcaatcaagaac	GGGACAAATAAAA	ATGtcttggg	
M2	taaaataaaaattt	GGGACAAATCATA	ATGtctcgca	
SH	aacacatcagagt	GGGATAAGTGACA	ATGataacat	
G	aaaacaaaaatat	GGGACAAAGTAGTT	ATGgaggtga	
L	aaacagcatccaa	GAGACAAATAGCA	ATGgatcctc	

CONSENSUS      ...at **GGGACAAAGTGAAA** **ATG**tctc...

gc A T A AGTT ga  
ta C C at

# Gene End Signal

	1	5	10
N	ttatg	AGTAATTAAAAAA	gt
P	tatgt	AGTTTAATAAAAA	taaaaaat
M	atttt	AGTTATATAAAAA	tcaagttagaat a
F	cagtt	AGTTAATTAAAAA	taaaataaaaatt t
M2	actta	AGTTAGTAAAAA	cacatcagagt
SH	agttt	AGTTATTTTAAAA	tatttgagaata g
G	aaatt	AGTTAACAAAAAA	tacgagatagct c
L	atgat	AGTTAATTAAAA	ttaaaaaattaaaa a

CONSENSUS      ...tt **AGTTAATTAAAAA** ta...

ag ATTAAT . cc  
ga GC gt

Fig. 8



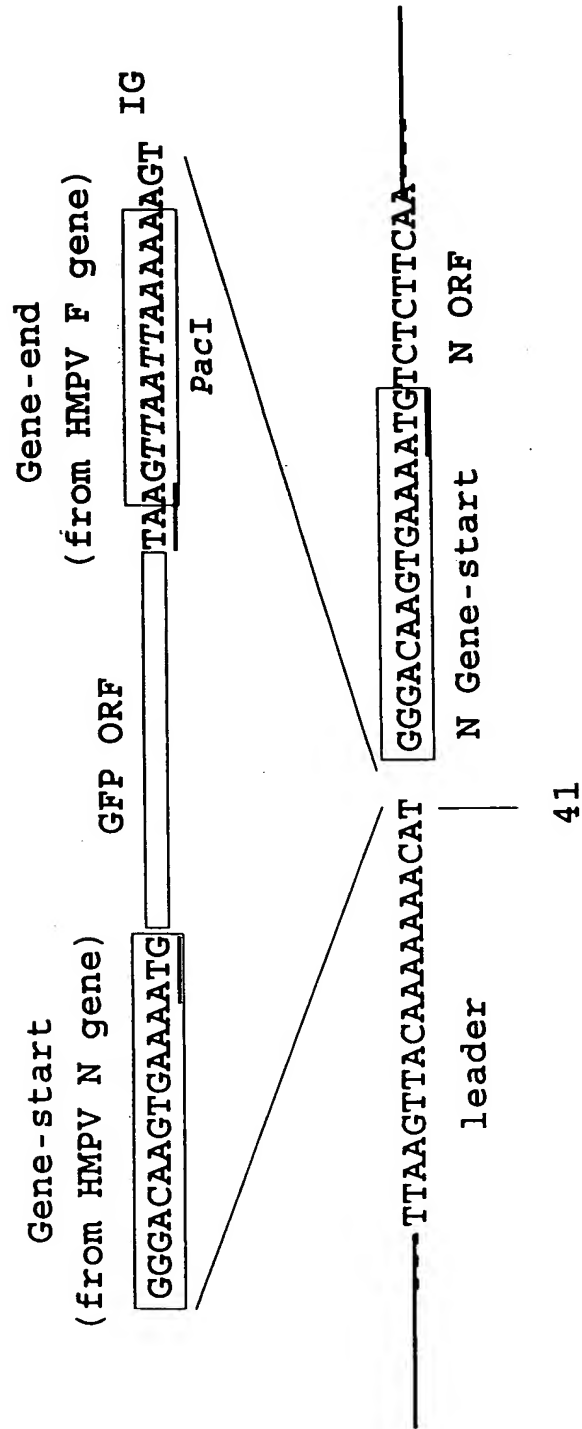


Fig. 9

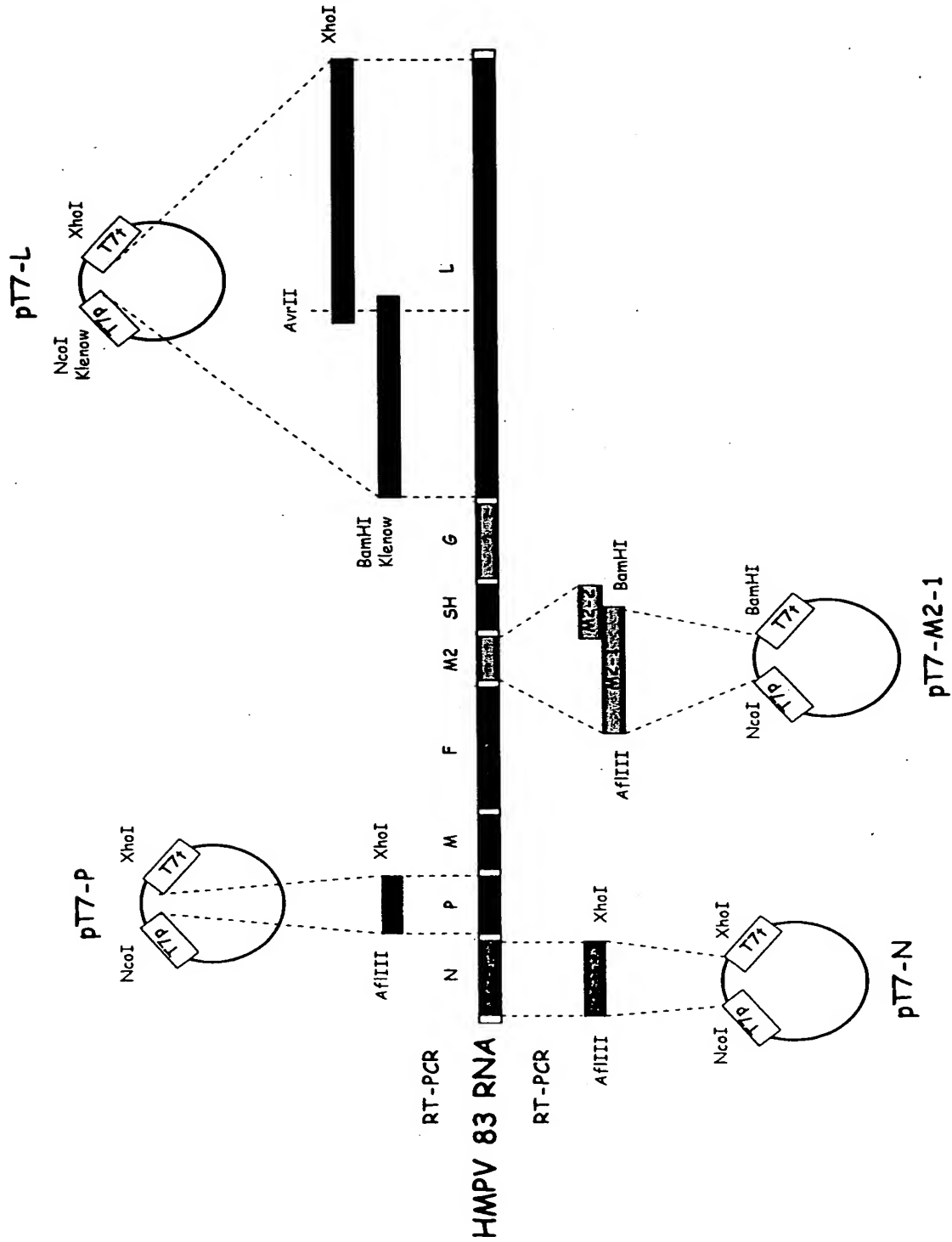


Fig. 10

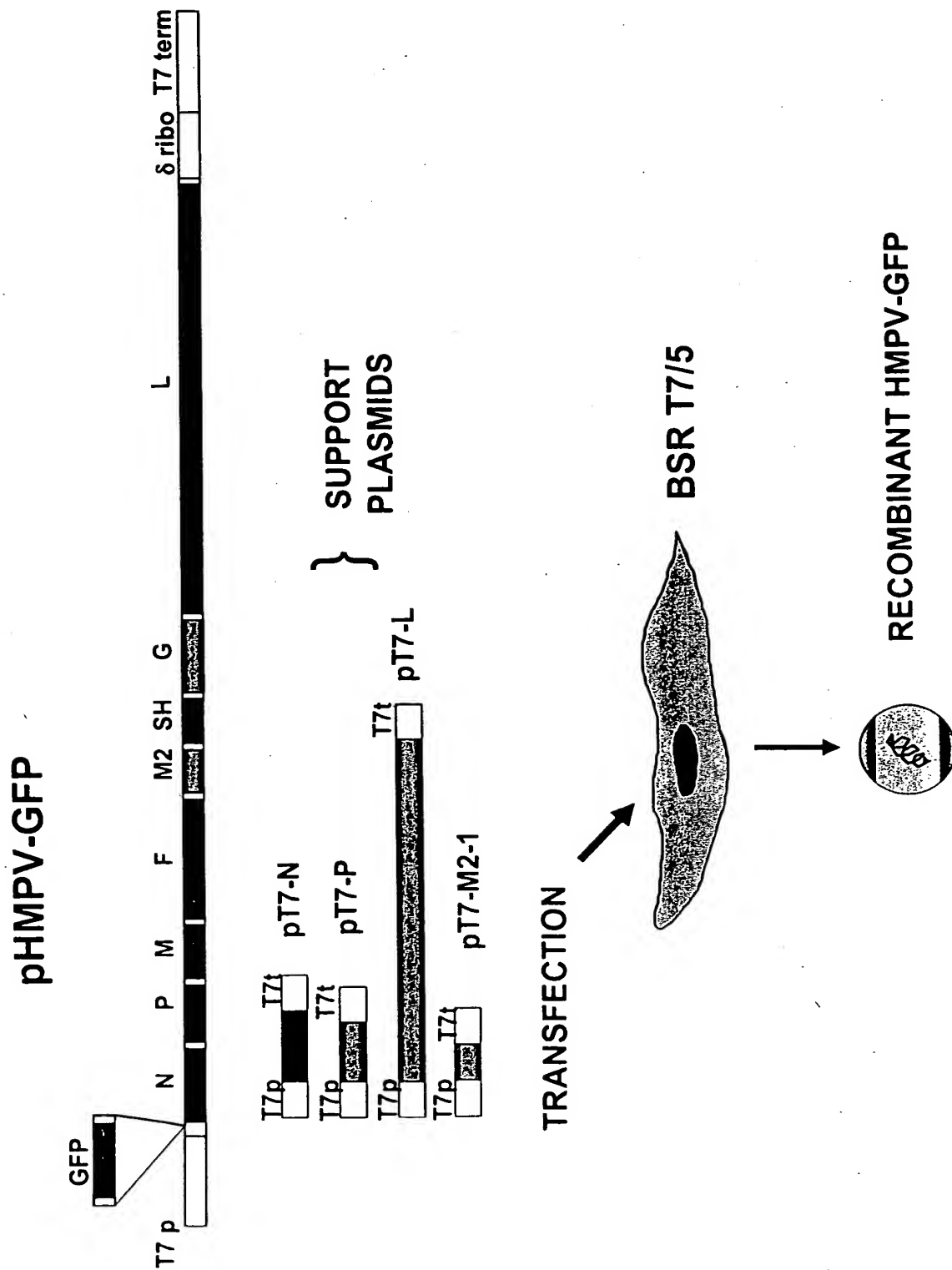


Fig. 11

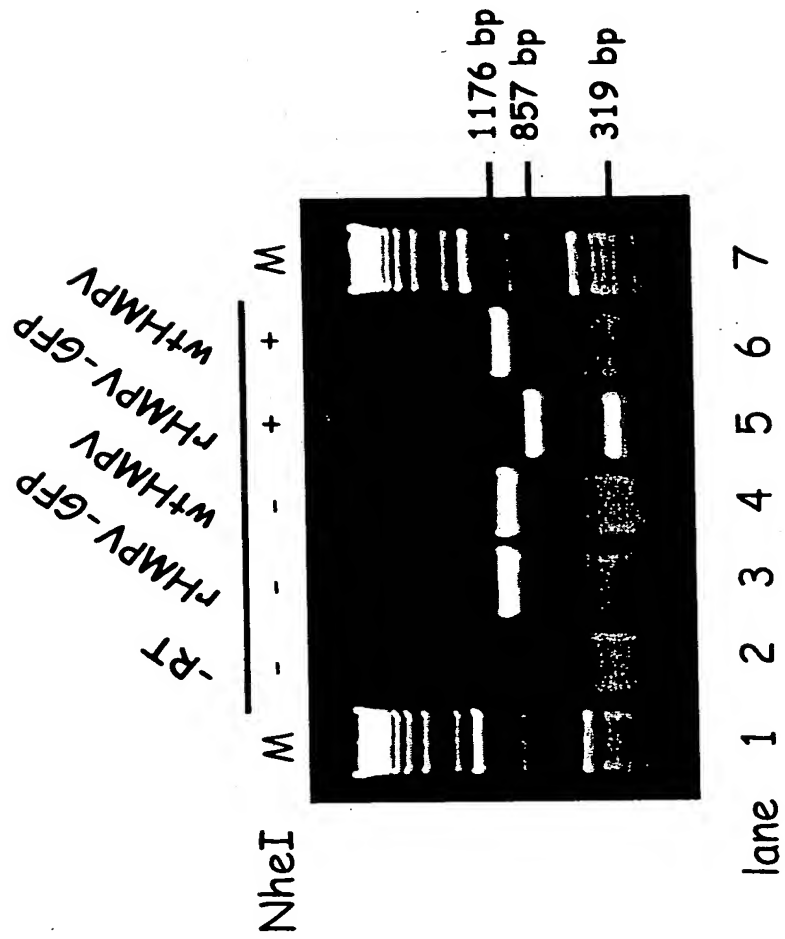


Fig. 12A

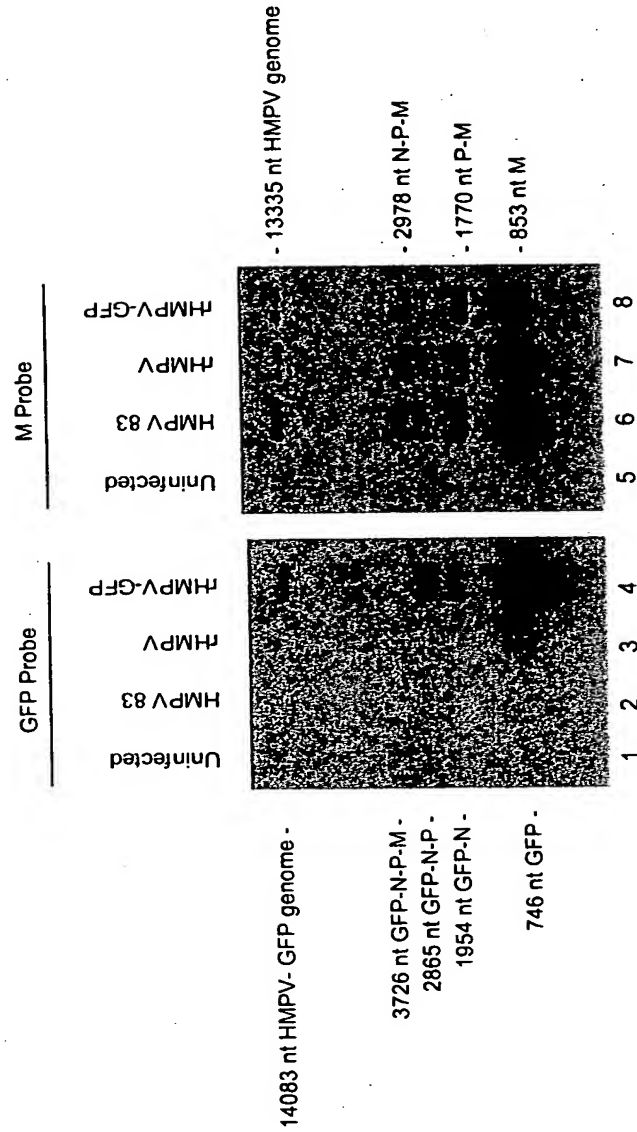


Fig. 12B

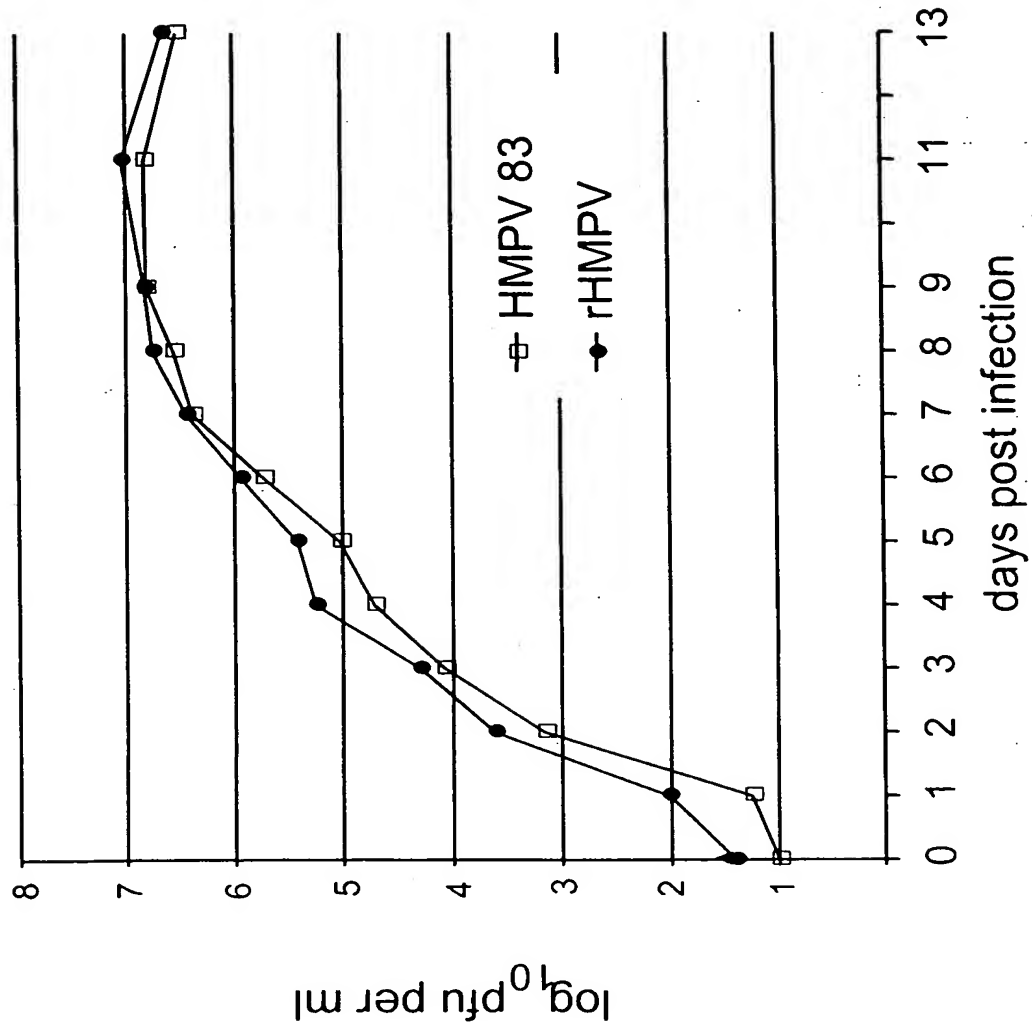


Fig. 13

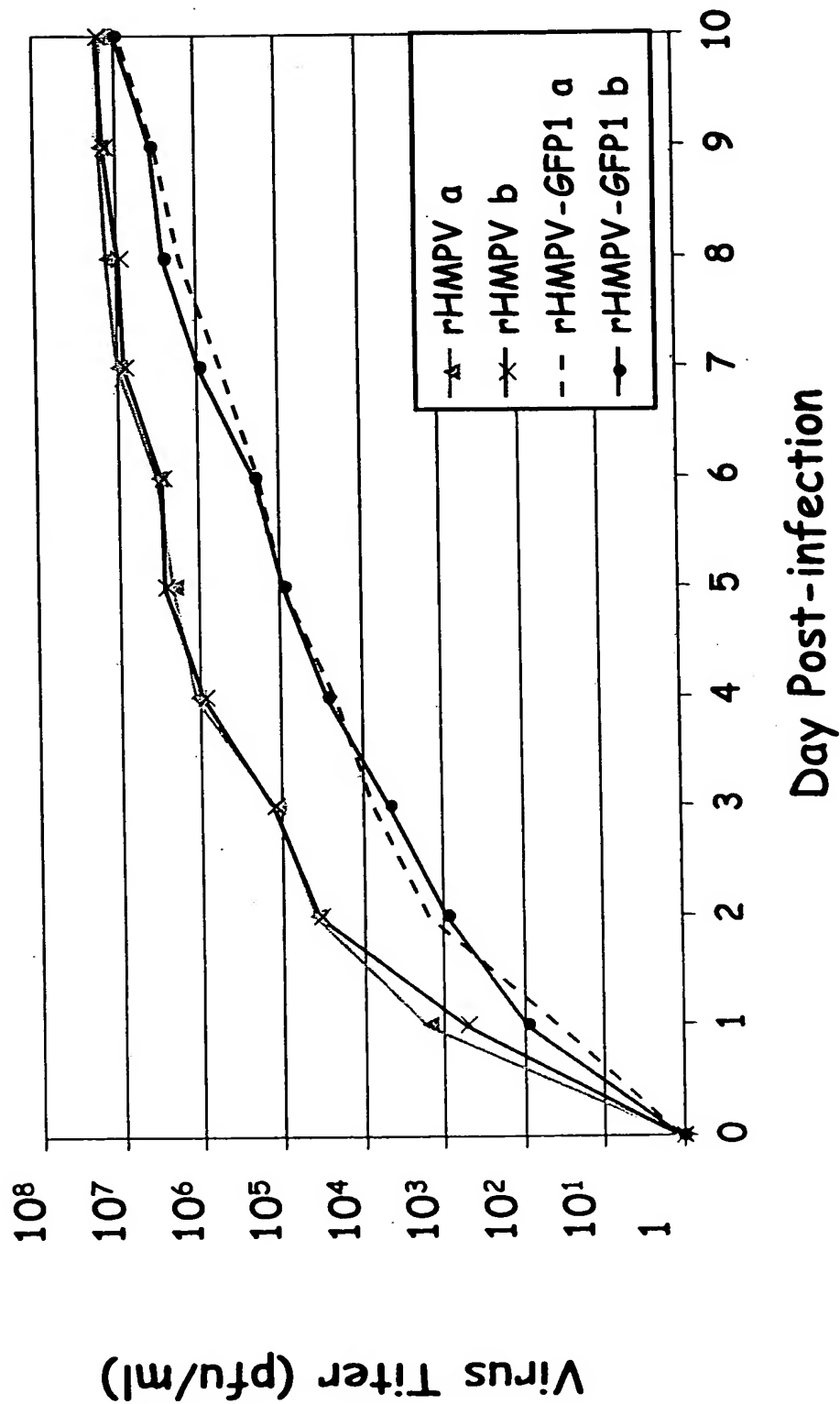


Fig. 14

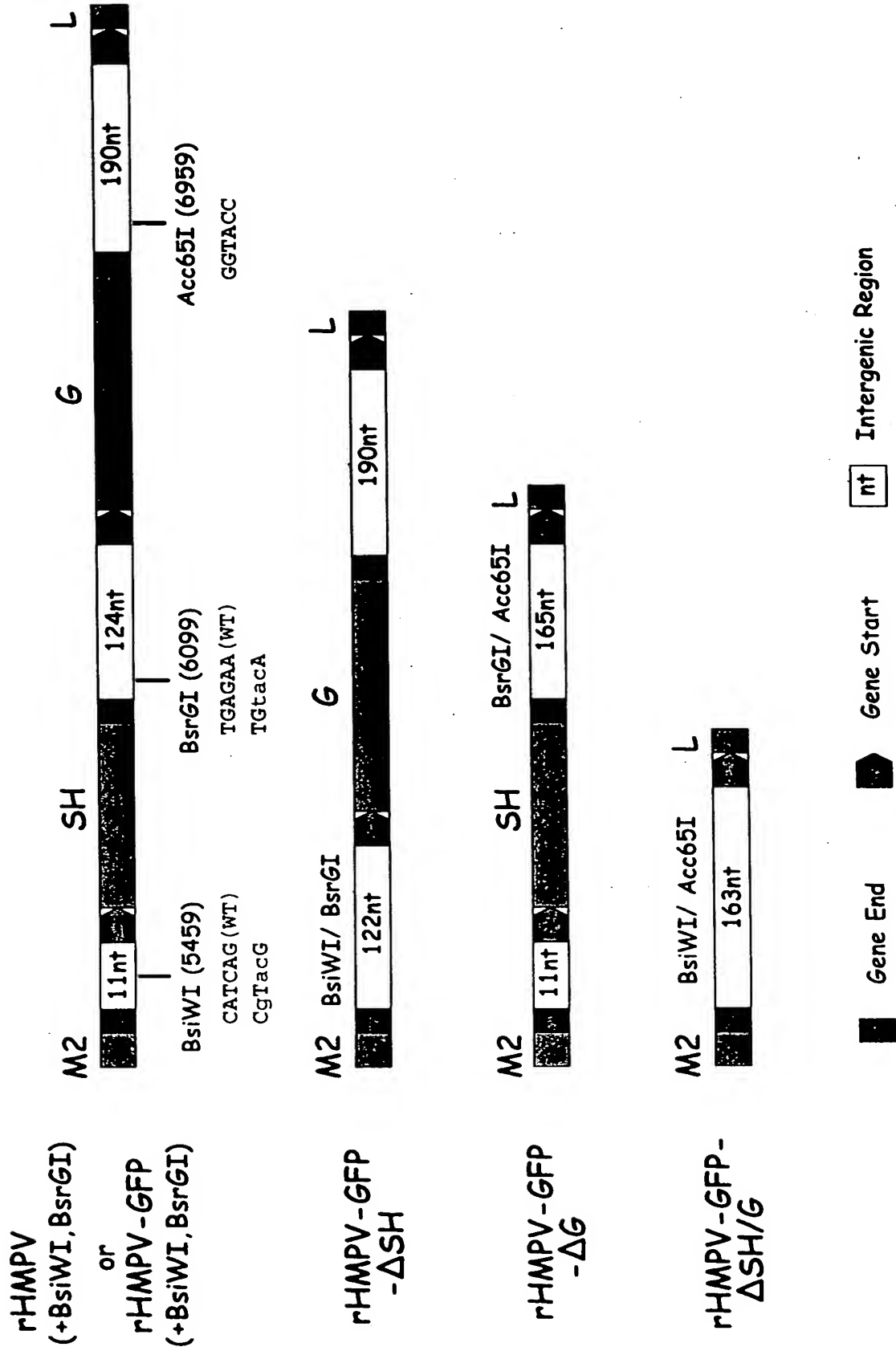


Fig. 15



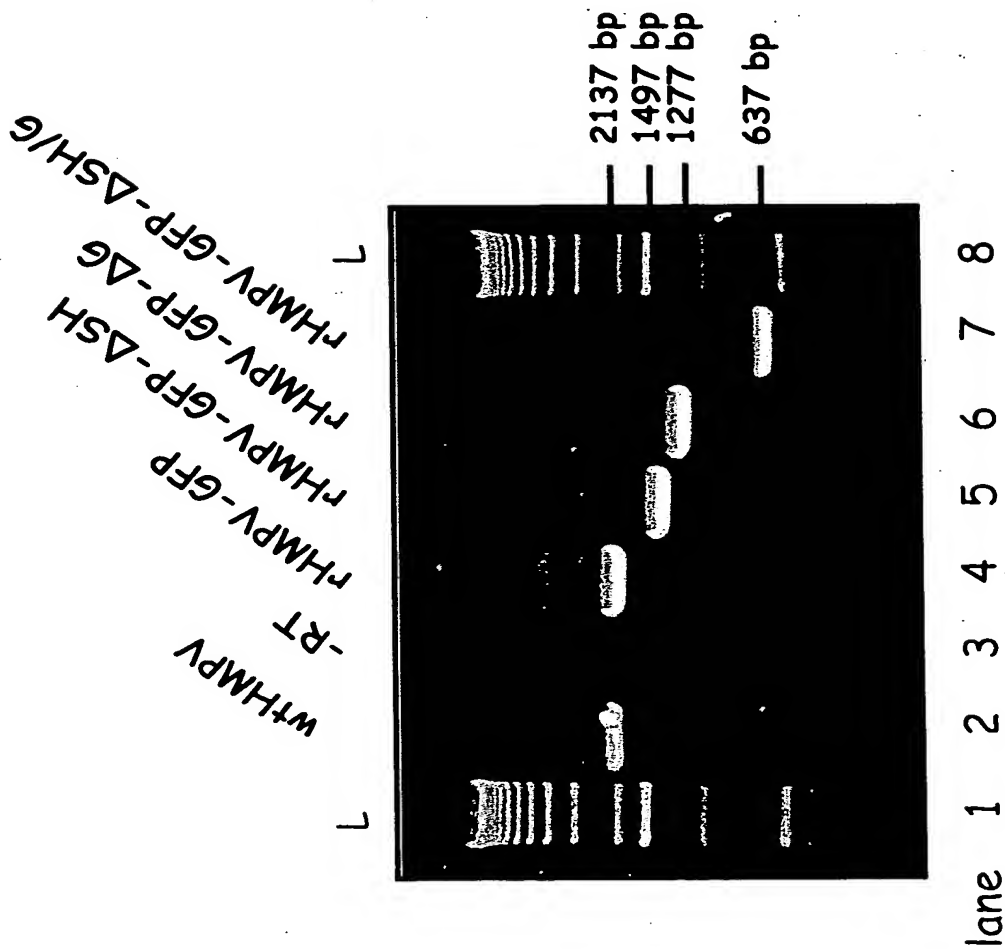


Fig. 16

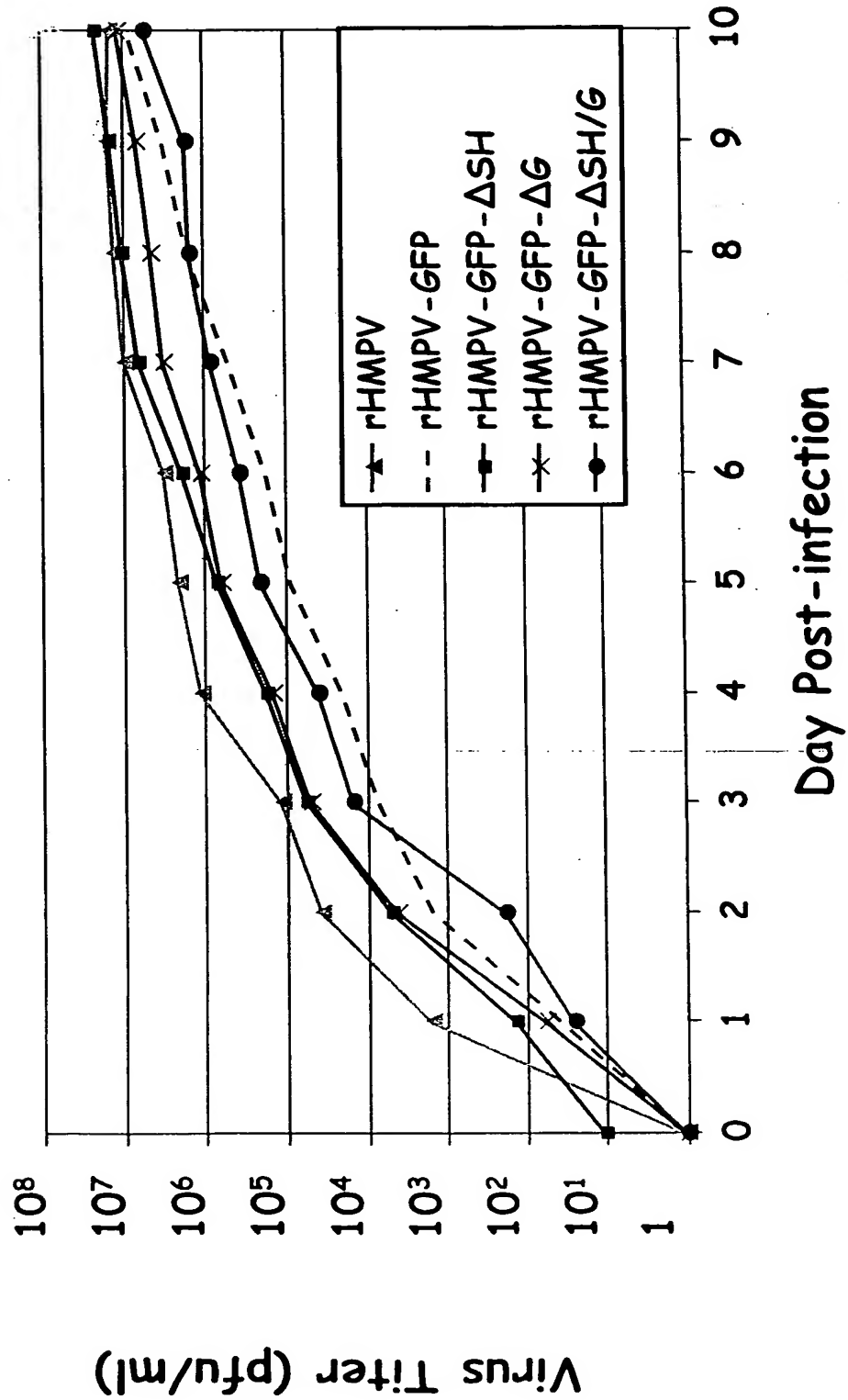


Fig. 17A

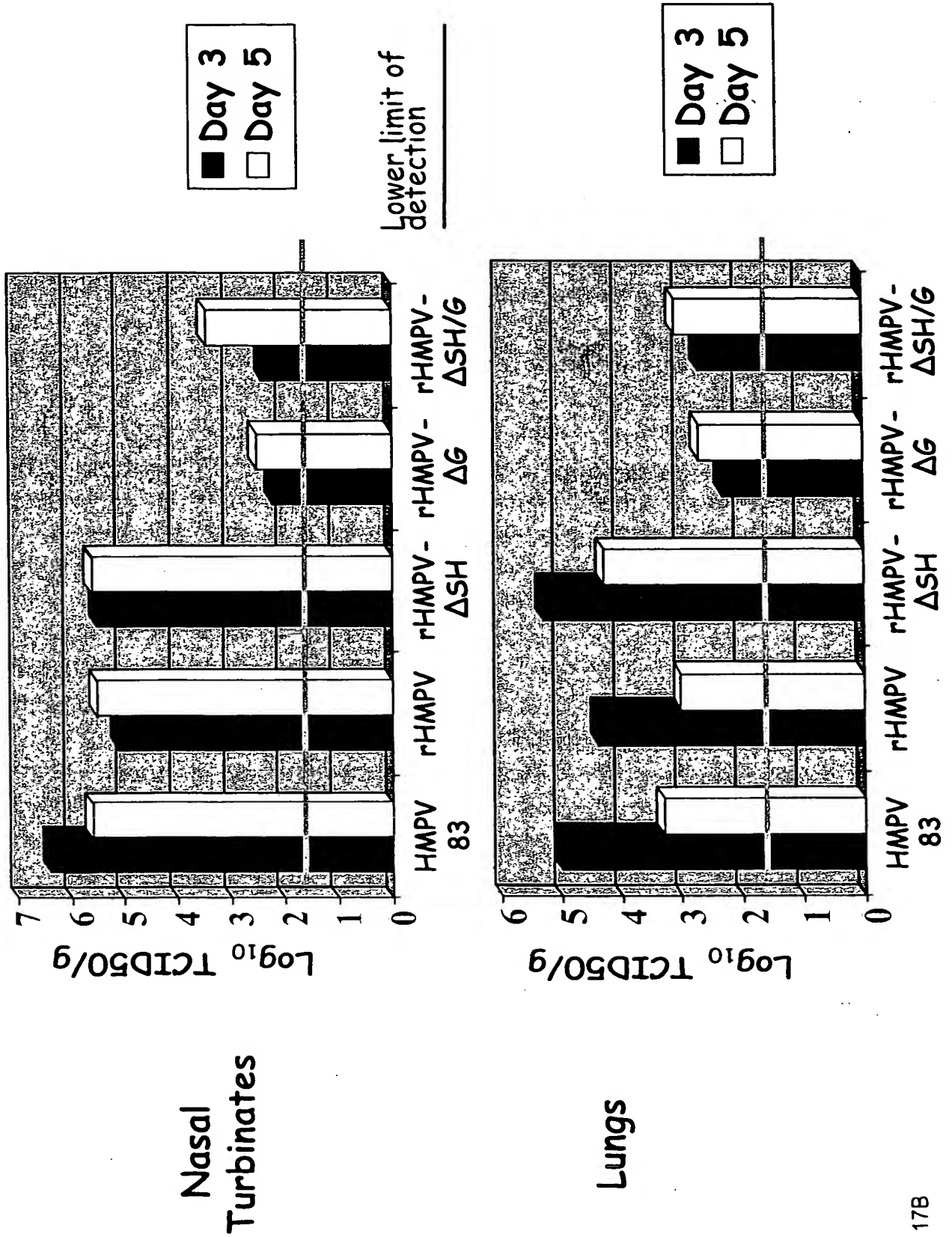


Fig. 17B

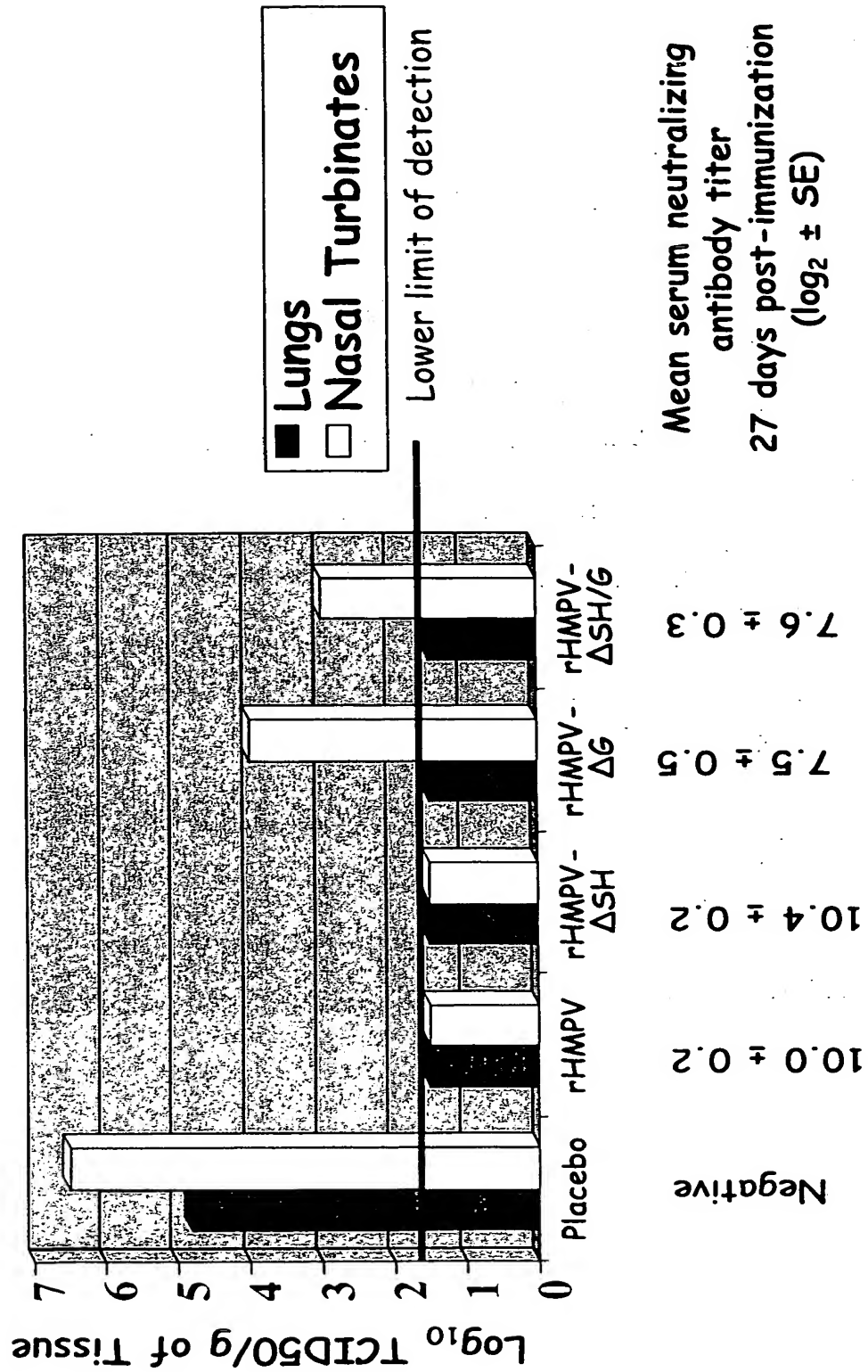


Fig. 17C

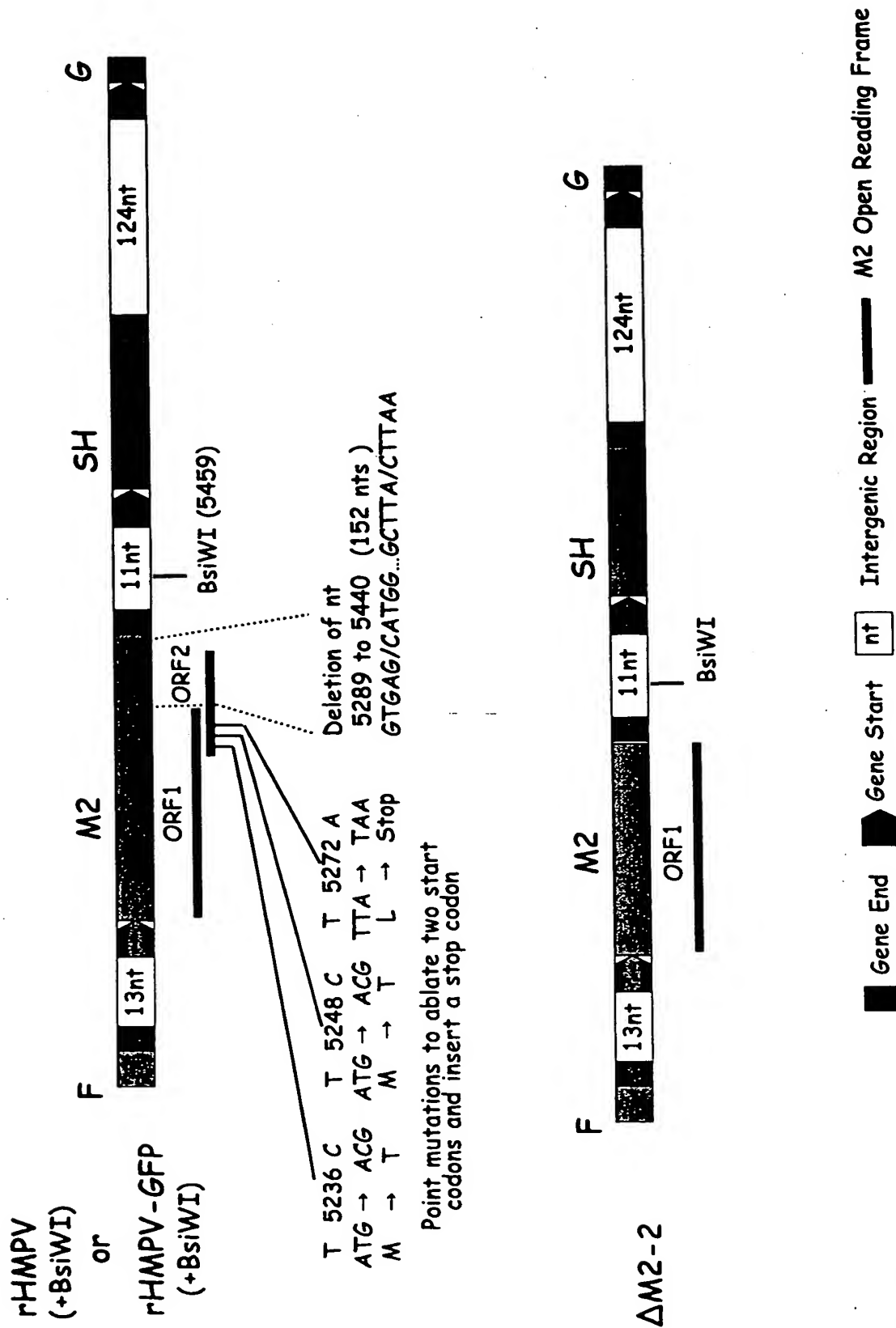


Fig. 18A

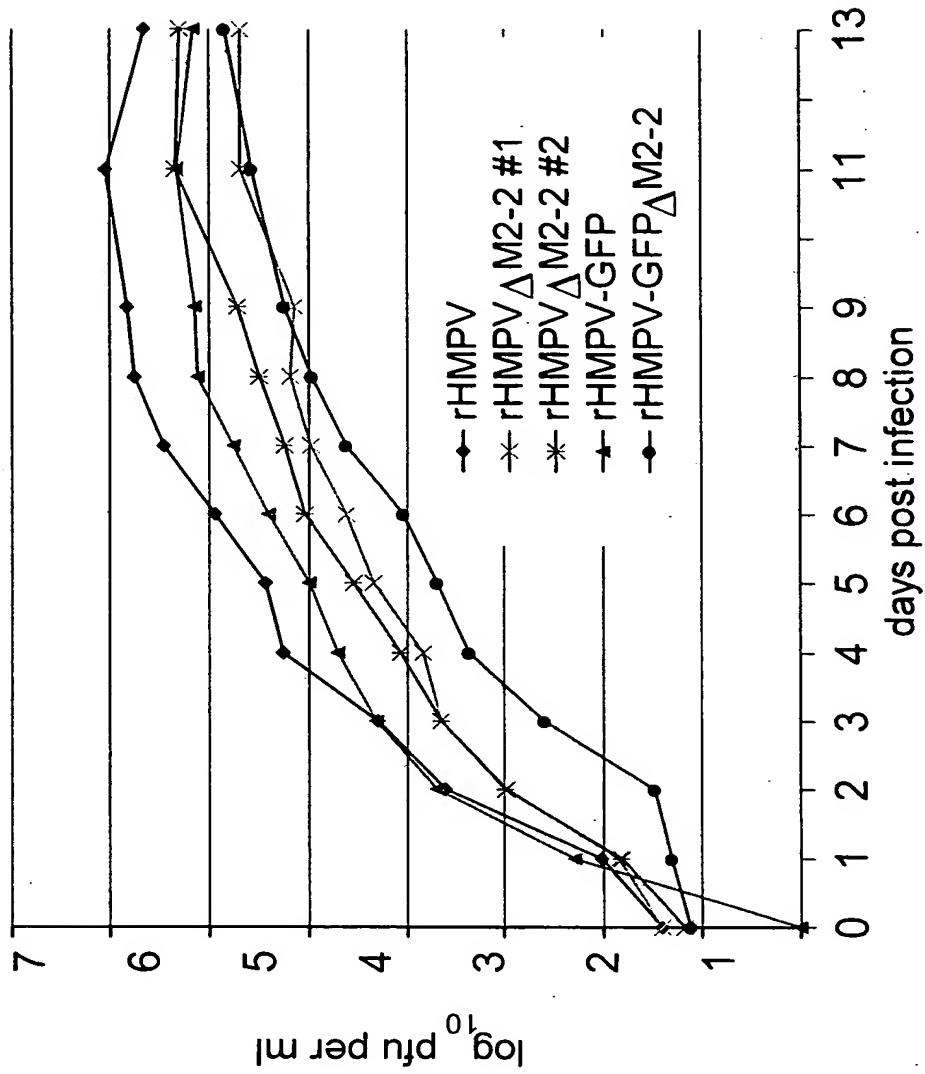


Fig. 18B

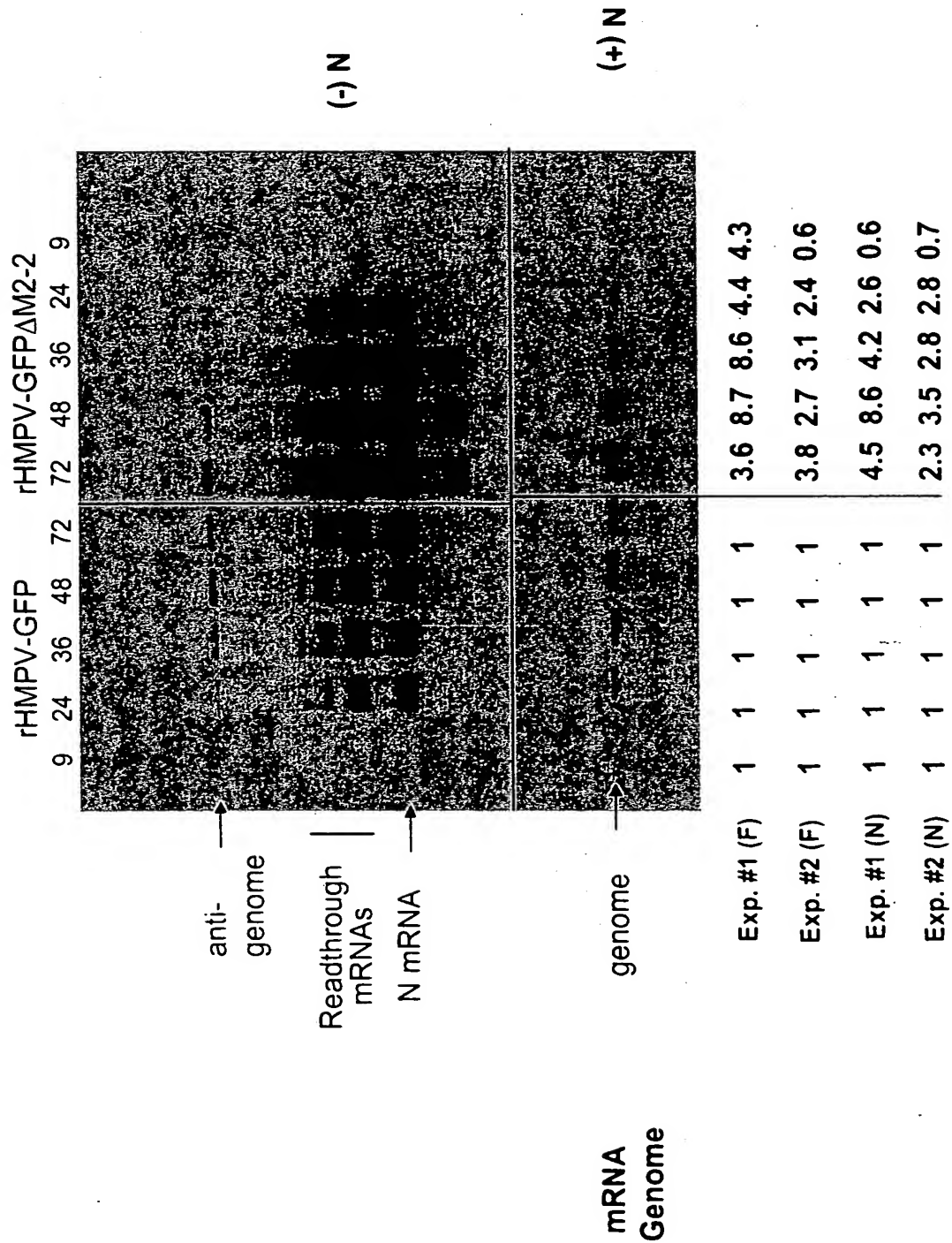


Fig. 18C





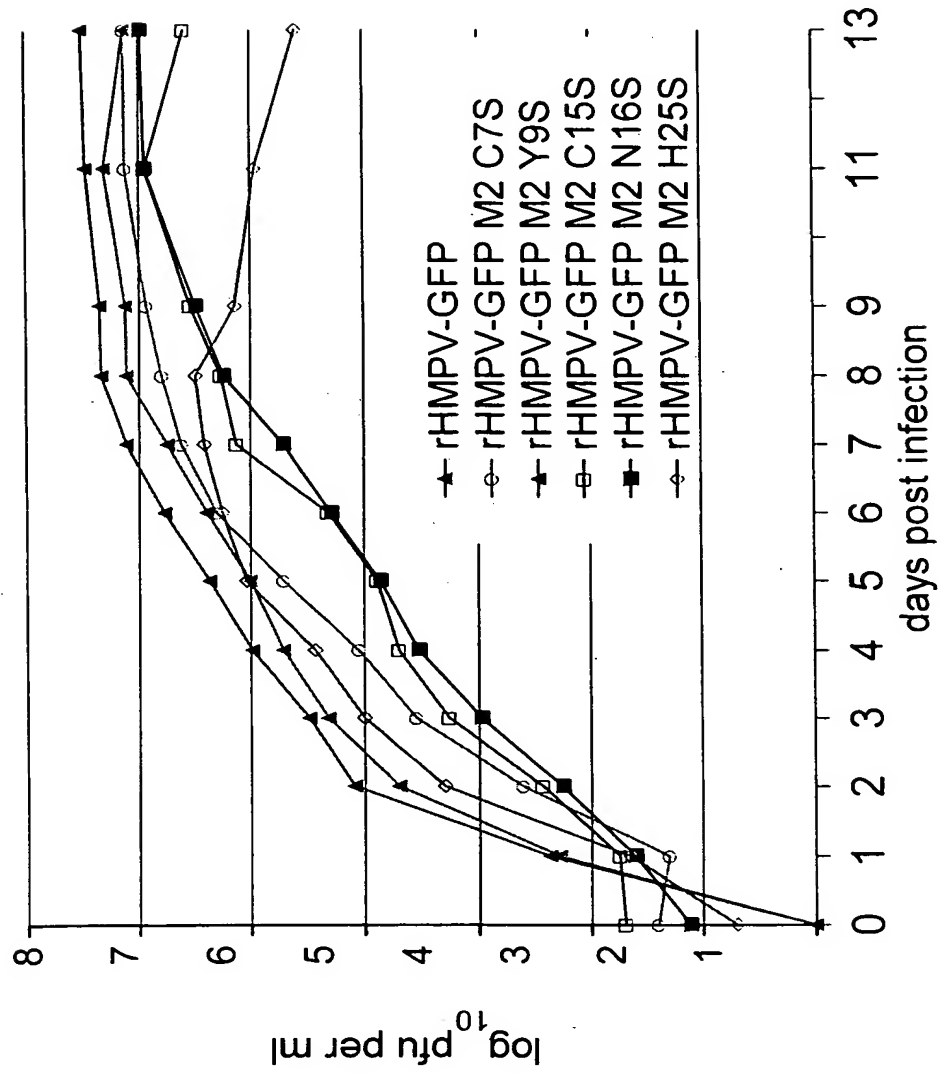


Fig. 20

	4711	GGGACAAATCATAATG	4775
HMPV		TCT CGC AAG GCT CCA TGC AAA TAT GAA GTG CGG GGC AAA	TGC AAC AGA
rHMPV-GFP ΔM2-1		tag	t aa
HMPV		M S R K A P C K Y E V R G K C N R	
rHMPV-GFP ΔM2-1		* * * * *	N N

Fig. 21

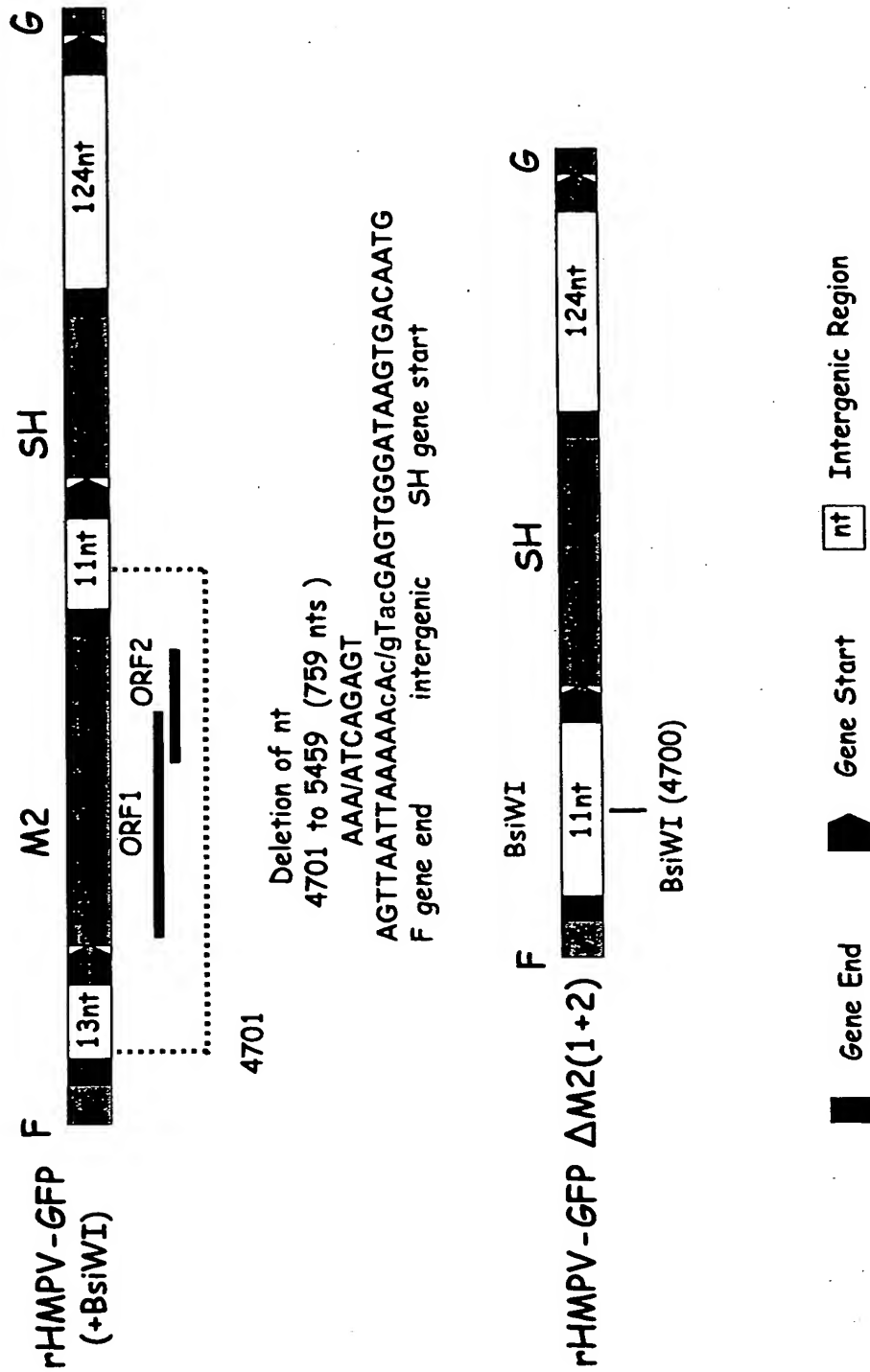


Fig. 22A

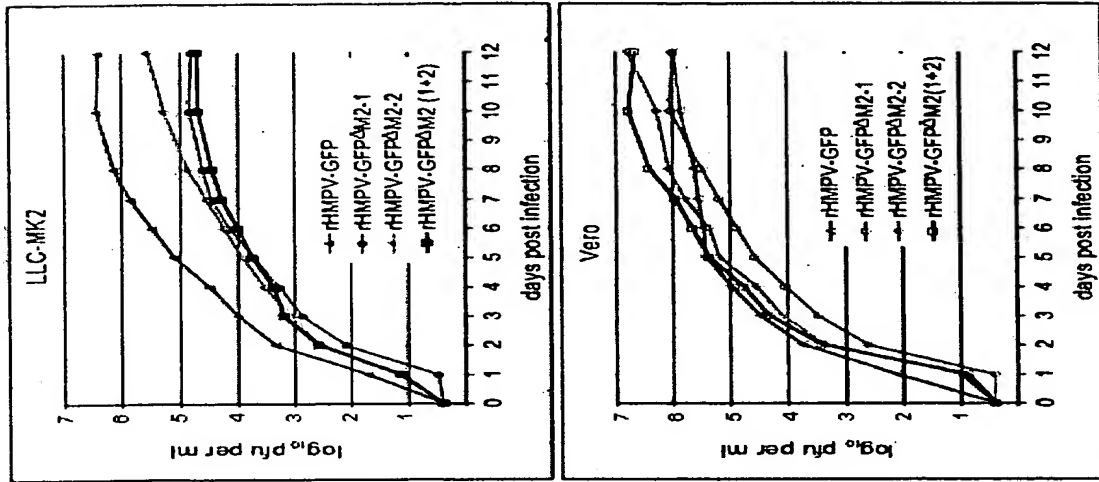


Fig. 22B

**Reduction of virus yield in presence of exogenous interferon (IFN) type I**

Virus	MOI	Fold reduction of virus yield		
		10 U IFN	100 U IFN	1000 U IFN
rHMPV-GFP	1.0	5	160	1680
rHMPV-GFP $\Delta$ M2(1+2)	1.0	19	1130	no virus
rHMPV-GFP $\Delta$ M2-2	1.0	13	250	no virus
RSV-GFP	0.01	4	17	90

Fig. 22C

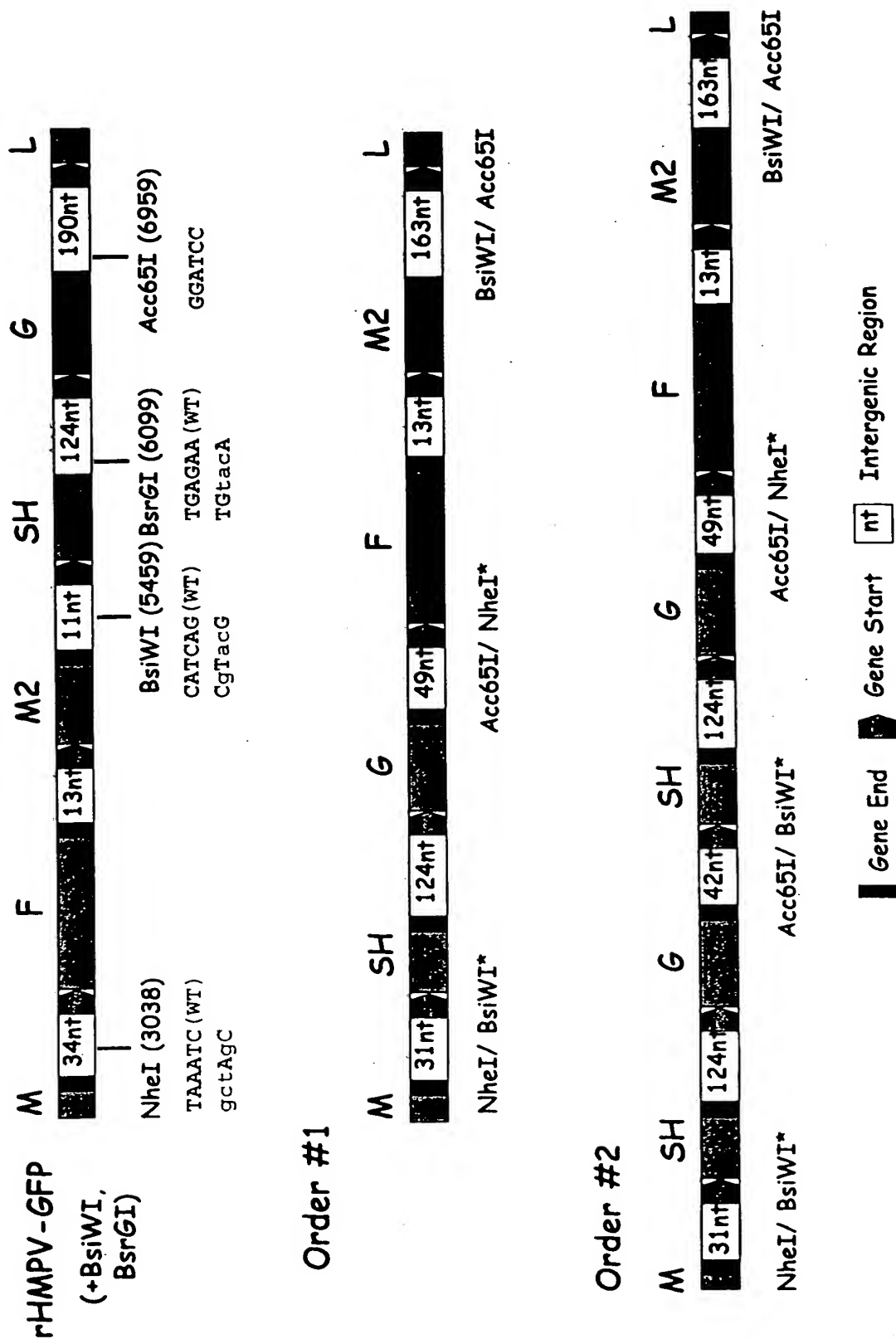


Fig. 23A

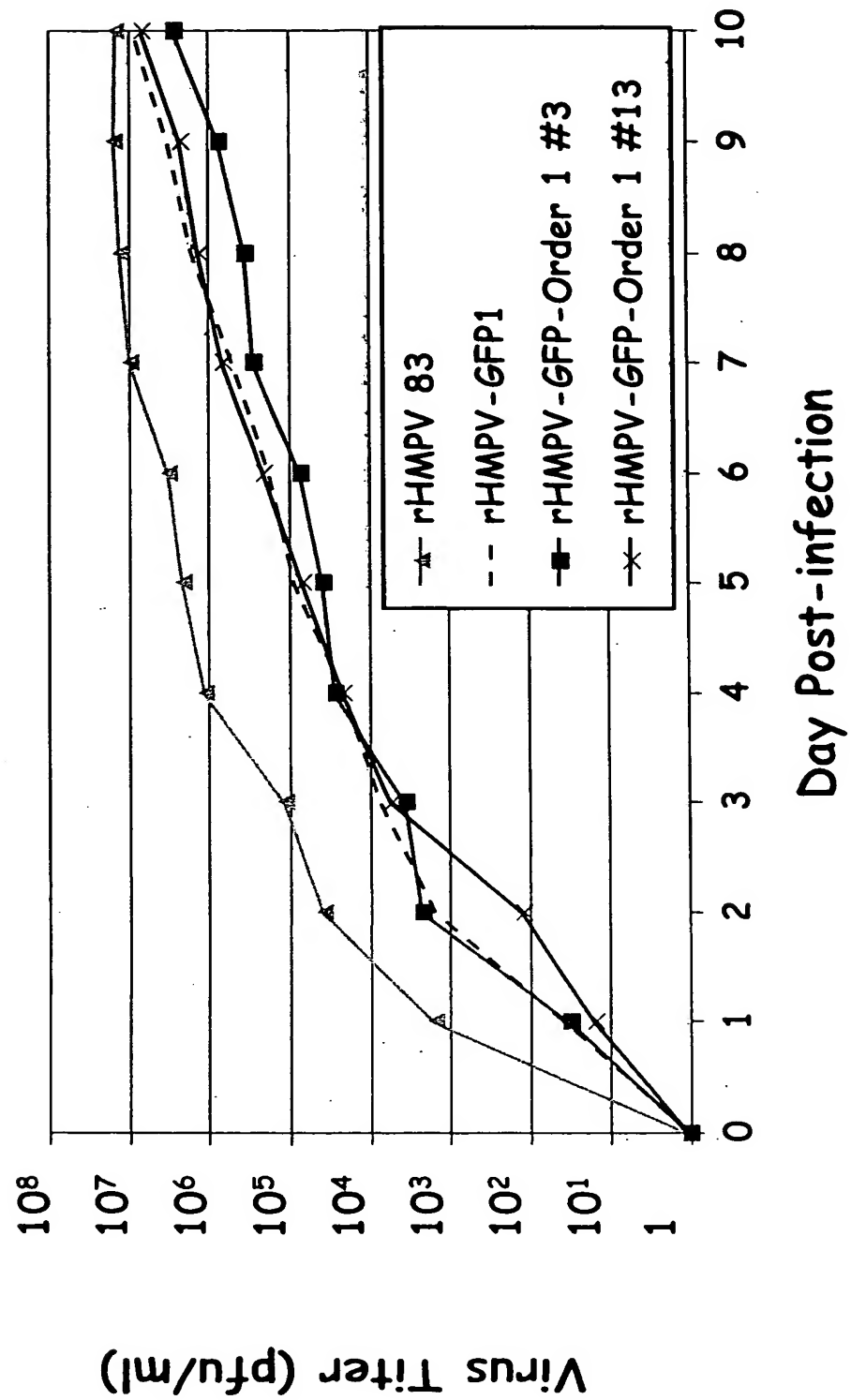


Fig. 23B

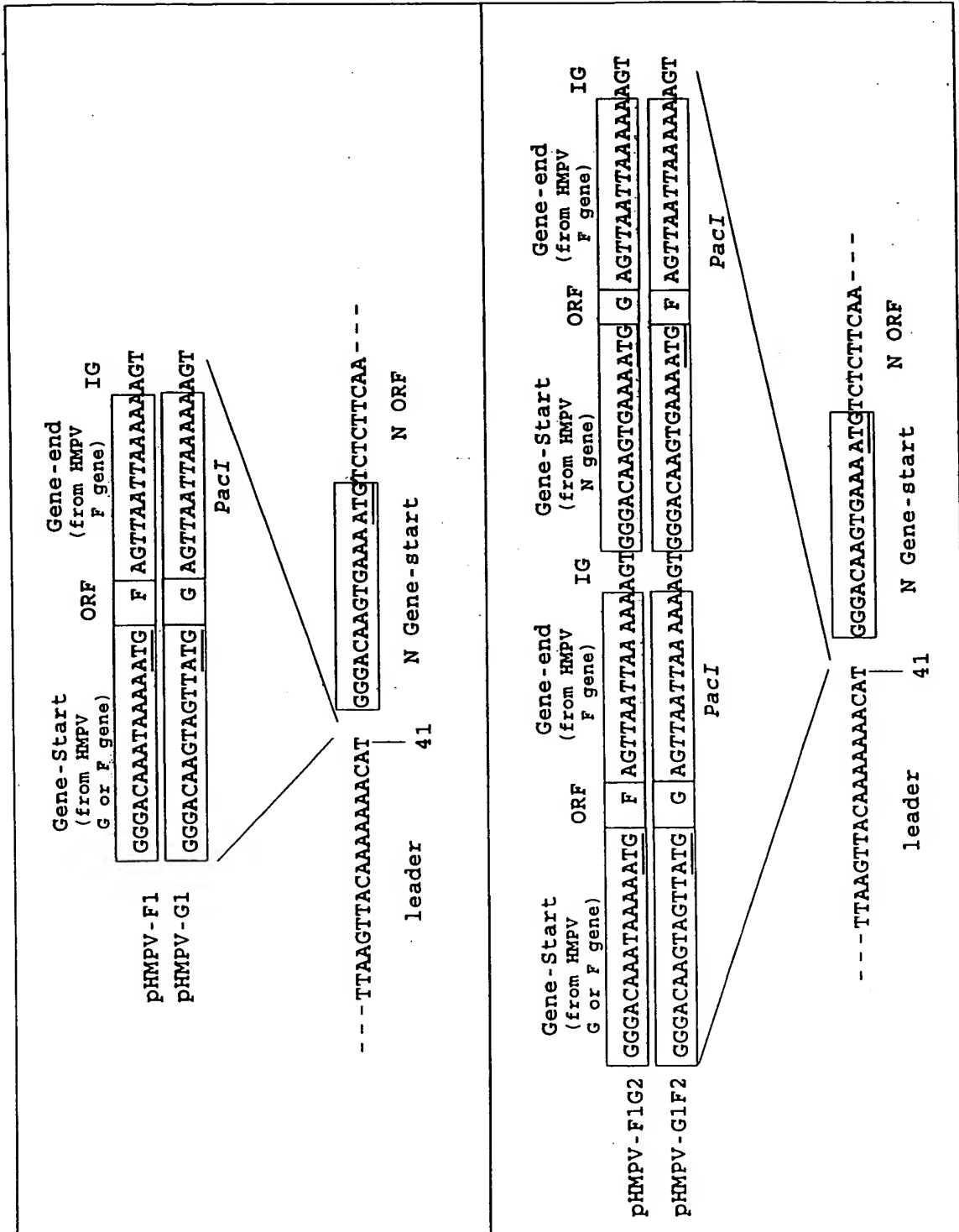


Fig. 24A



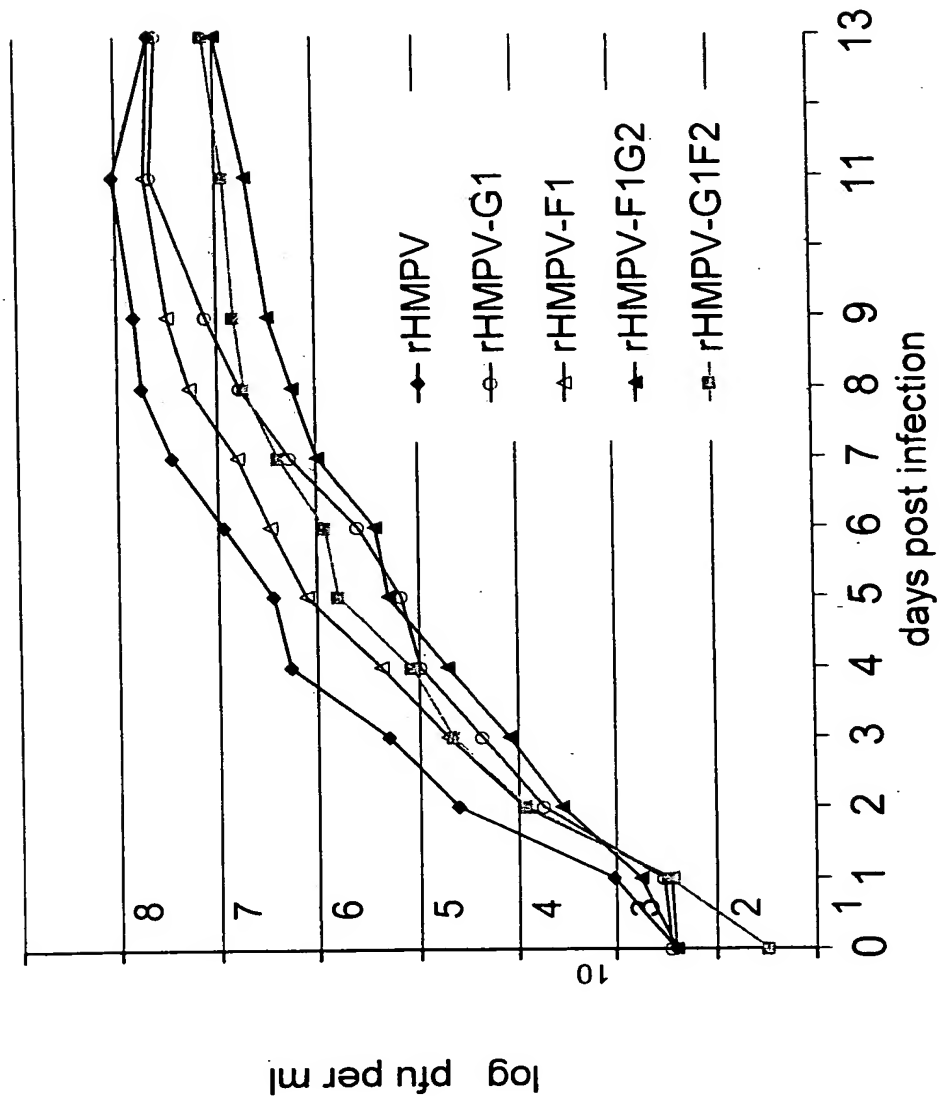


Fig. 24B

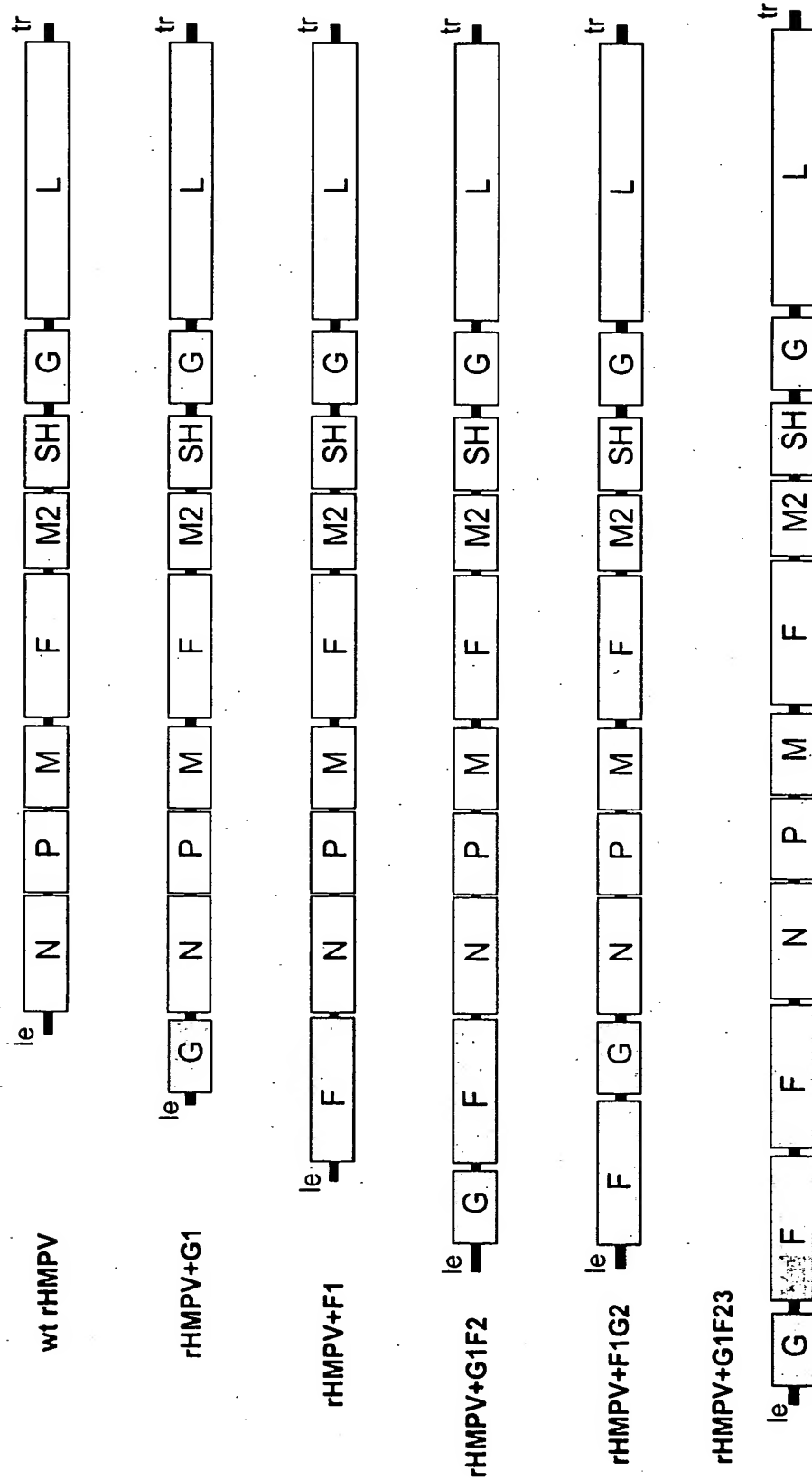


Fig. 25A

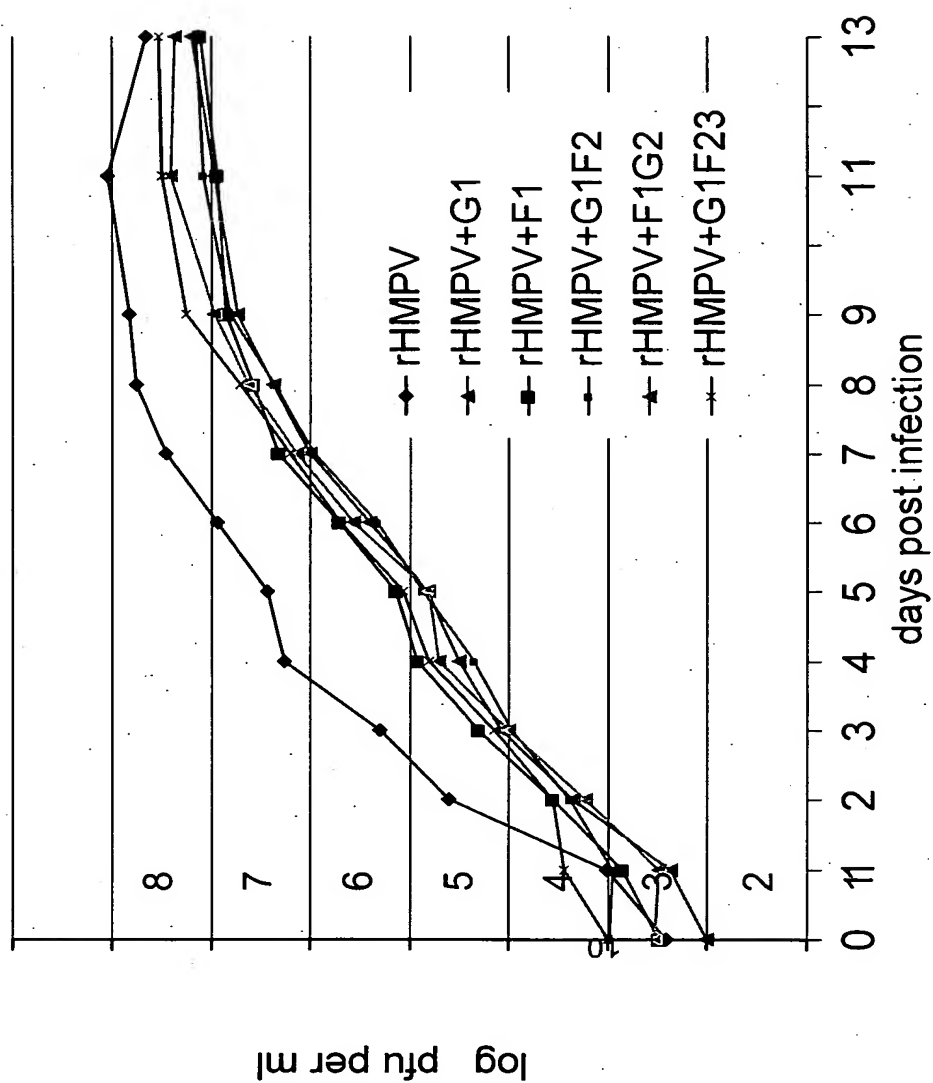


Fig. 25B

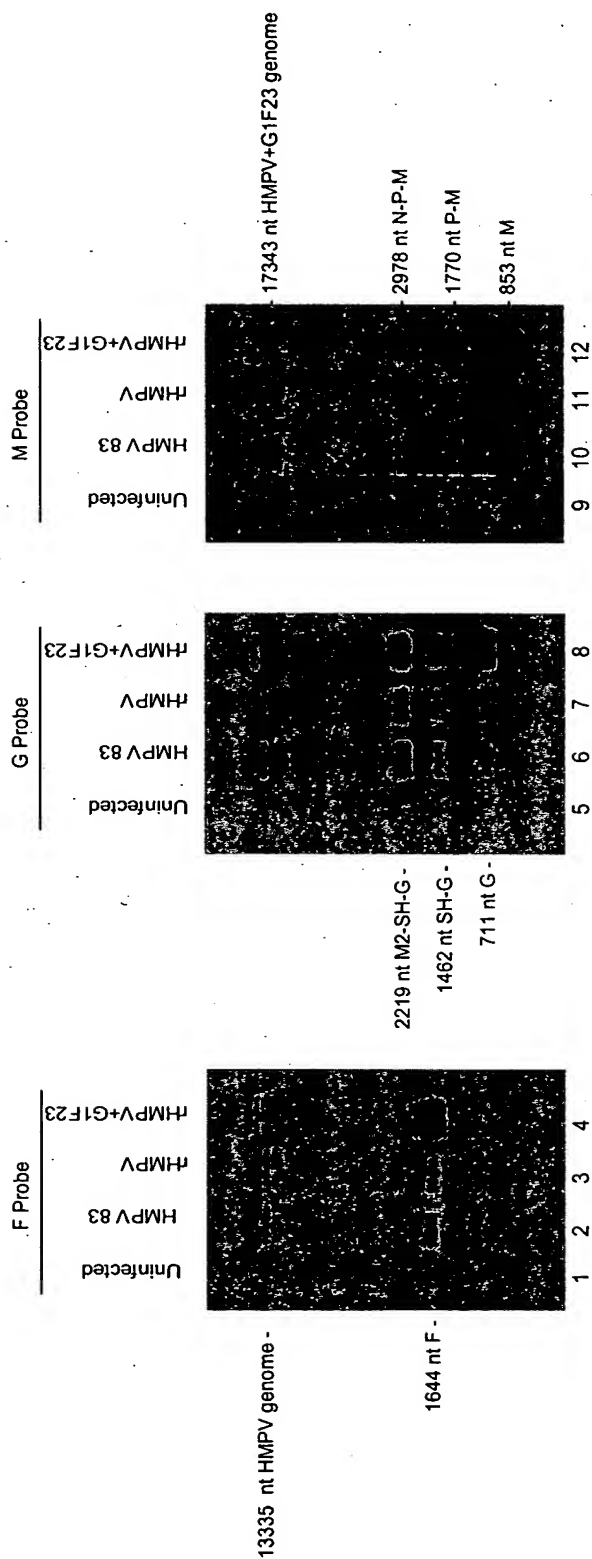


Fig. 25C

# RSV A2 Mutations F521L and AA8

## F521L (RSV)

hRSV A2	507	E	L	T	E	R	D	L	I	V	L	S	G	L	R	F	Y	R	E	F	R	L	P	K	K	V	D	L	E	M	I	I	N	D	K	A	I	S	P	P	K	N	L	I	W	T	-	S	F	P	R	
hPIV3	442	E	N	A	V	D	Y	Y	Q	S	S	F	I	G	I	K	F	N	K	F	I	E	P	Q	L	D	E	D	L	T	I	Y	M	K	D	K	A	L	S	P	P	K	-	S	N	W	D	T	V	Y	P	A
hPIV1	442	E	C	A	V	D	N	Y	S	S	F	I	G	F	K	F	L	K	F	I	E	P	Q	L	D	E	D	L	T	I	Y	M	K	D	K	A	L	S	P	P	R	K	-	A	A	W	D	S	V	Y	P	D
hMPV 83	442	E	L	S	E	Q	D	F	L	E	L	A	A	I	Q	F	F	E	Q	E	F	S	V	P	E	K	T	N	L	E	M	V	L	N	D	K	A	I	S	P	P	K	R	L	I	W	S	-	V	Y	P	K
hMPV 001	442	E	L	S	E	Q	D	F	L	E	L	A	A	I	Q	F	F	E	Q	E	F	S	V	P	E	K	T	N	L	E	M	V	L	N	D	K	A	I	S	P	P	K	R	L	I	W	S	-	V	Y	P	K

456

hRSV A2	593	N	Y	M	P	S	H	I	Q	N	Y	I	E	H	E	K	L	K	F	S	E	S	D	K	S	R	R	V	L	E	Y	Y	L	R	D	N	K	F	N	593
hPIV3	517	-	-	-	-	-	-	S	N	-	-	-	-	L	L	Y	R	T	N	A	S	N	E	S	R	R	L	V	E	V	F	I	A	D	S	K	F	D	517	
hPIV1	517	-	-	-	-	-	-	S	N	-	-	-	-	L	Y	Y	K	V	P	E	S	E	E	T	R	R	L	I	E	V	F	I	N	D	N	F	N	517		
hMPV 83	528	N	Y	L	P	E	T	I	K	N	R	Y	L	E	E	T	F	N	A	S	D	S	L	K	T	R	R	V	L	E	Y	Y	L	K	D	N	K	F	D	528
hMPV 001	528	N	Y	L	P	E	K	I	K	N	R	Y	L	E	E	T	F	N	A	S	D	S	L	K	T	R	R	V	L	E	Y	Y	L	K	D	N	K	F	D	528

456

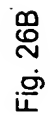
hRSV A2	593	N	K	F	N	D	R	L	E	V	R	R	R	S	K	D	N	K	F	N	593
hPTV3	517	D	S	K	F	D	I	A	V	E	L	V	E	S	R	R	L	N	E	517	
hPTV1	517	N	N	F	N	D	I	N	V	F	I	E	V	E	T	R	R	L	E	517	
hMPV 83	528	L	K	D	N	K	F	D	V	L	E	V	L	S	D	S	L	K	T	528	
hMPV 001	528	L	K	D	N	K	F	D	V	L	E	V	L	S	D	S	L	K	T	528	

R588A  
D589A

AA8 (double amino  
acid substitution)

R588A  
 D589A  
 AA8 (double amino acid substitution)

Fig. 26A



## BPIV3 Mutation I1103V

I1103V

hPIV3	1087	R	V	G	I	S	R	R	G	-	G	L	T	Y	N	L	L	R	K	I	S	N	Y	D	L	V	Q	Y	E	T	L	S	1115
hPIV3	1087	R	V	G	I	N	R	R	G	-	G	L	T	Y	N	L	L	R	K	I	S	N	Y	D	L	V	Q	Y	E	T	L	S	1115
hPIV1	1087	R	A	S	V	R	R	G	-	G	L	T	Y	N	L	L	R	R	L	I	N	Y	D	L	L	L	Q	Y	E	T	L	S	1115
hRSV A2	1153	K	T	S	A	I	D	L	T	D	I	D	R	A	T	E	M	M	R	K	N	I	T	L	L	L	I	R	I	L	P	L	1182
hMPV 83	1078	R	T	S	A	I	N	G	E	D	I	D	R	A	V	S	M	M	L	E	N	L	G	L	L	L	S	R	I	L	S	V	1107
hMPV 001	1078	R	T	S	A	I	N	G	E	D	I	D	R	A	V	S	M	M	L	E	N	L	G	L	L	L	S	R	I	L	S	V	1107

## HPIV3 Mutation T1558I

T1558I

hPIV3	1539	K	V	F	K	R	F	F	W	D	C	G	V	L	N	P	I	Y	G	P	N	T	A	S	Q	D	Q	I	K	L	A	L	S	I	C	E	1572	
hPIV1	1539	K	I	F	K	R	F	W	D	A	G	V	V	V	E	P	V	Y	G	P	N	L	S	N	Q	D	Q	K	I	L	L	A	L	S	V	C	E	1572
hRSV A2	1586	K	V	I	K	Y	I	L	S	Q	D	A	D	V	S	L	H	R	V	K	G	C	H	S	F	K	L	W	F	L	K	R	L	N	V	A	E	1619
hMPV 83	1507	K	V	K	K	R	I	M	L	Y	D	V	V	K	F	L	S	L	V	G	Y	I	G	F	K	N	W	F	F	E	Q	L	L	R	S	A	E	1540
hMPV 001	1507	K	V	K	K	R	I	M	L	Y	D	V	V	K	F	L	S	L	V	G	Y	I	G	F	K	N	W	F	F	E	Q	L	L	R	S	A	E	1540

## RSV A2 Mutation C319Y

C319Y

hPIV3	258	K	L	Q	S	M	Y	Q	K	G	N	N	L	W	E	V	I	D	K	L	F	P	I	M	G	E	K	T	F	D	V	I	288	
hPIV1	258	R	S	S	K	I	T	C	K	G	E	E	L	W	E	L	V	I	D	S	L	F	P	N	L	G	E	D	V	N	I	I	288	
hRSV A2	302	R	C	G	F	N	N	V	I	L	T	Q	L	F	L	Y	G	D	C	I	L	K	L	F	H	N	E	G	F	S	Y	I	I	332
hMPV 83	239	R	S	N	L	Q	G	M	L	T	N	K	L	L	Y	E	T	V	D	Y	M	L	S	L	C	C	N	E	G	F	S	L	V	269
hMPV 001	239	R	S	N	L	Q	G	I	L	T	N	K	L	L	Y	E	T	V	D	Y	M	L	S	L	C	C	N	E	G	F	S	L	V	269

Fig. 26C

# RSV A2 Mutation Q831L

hPIV3	772	G D N Q A I A V T T R V P N N Y D Y R I K K E I V Y K D D V V R F F D S L R E V M D D L G H	816
hPIV1	772	G D N Q A I A V T T S R V P V T Q T Y K Q K K T H V Y E E I T R Y F G A L R E V M F D I G H	816
hRSV A2	810	G D N Q S I D I S K P I R L M E G Q T - H A Q A D Y L L L A L N S L K L L Y K E Y A G I G H	853
hMPV 83	744	G D N Q S I D V S K P V K L S E G L D - E V K A D Y R L A V K M L K K E T R D A Y R N I G H	787
hMPV 001	744	G D N Q S I D V S K P V K L S E G L D - E V K A D Y S L A V K M L K K E T R D A Y R N I G H	787

# RSV A2 Mutations M1169V, D1183E and C9

hPIV3	1087	R V G I N R R G - G L T Y S L L R K I S N Y D L V Q Y E T L S R T L R	D1183E
hPIV1	1087	R A S V R R G - G L S Y S I L R R L I N Y D L L Q Y E T L T R T L R	
hRSV A2	1153	K T S A I D L T I D R A T E M M R K E N L G G L L L R I L P L D C N R	
hMPV 83	1078	R T S A I N G E D I D R A V S M M L E N L G G L L L R I L S V V V D S	
hMPV 001	1078	R T S A I N G E D I D R A V S M M L E N L G G L L L R I L S V V V D S	

hPIV3	1160	L I V S D K I R Y E D M C S V D L A I A L R Q K M W I H L S G G R M I S G L E T P	1160
hPIV1	1160	K P V K D N I E Y E Y M C S V E L A I G L R Q K M W F H L T Y G R P I H G L E T P	1160
hRSV A2	1222	D K R E I L S M E N L S I - T E L S K Y Y V R E R S W S L S N - - - I V G V T S P	1222
hMPV 83	1147	I E I P I K S N G R L I C - C Q I S R T L R E T S W N N M E - - - I V G V T S P	1147
hMPV 001	1147	I E I P I K S N G R L I C - C Q I S R T L R E T S W N N M E - - - I V G V T S P	1147

D1187A\* R1189A\*  
 K1188A\* E1190A\*  
 E1208A\* R1209A\*

\* Six point mutations collectively designated C9





# RSV A2 Mutation N43I

hPTV3	24	I	V	K	G	K	I	A	Q	L	H	T	I	M	S	L	P	Q	P	Y	D	M	D	D	S	I	L	V	I	52	
hPTV1	24	I	V	K	S	K	I	A	Q	L	H	V	L	L	D	I	N	Q	P	Y	D	L	K	D	N	S	I	I	N	I	52
hRSV A2	23	I	S	F	S	E	C	N	A	L	G	S	Y	I	-	F	N	G	P	Y	L	K	N	D	Y	T	N	L	I	S	50
hMPV 83	22	I	S	F	S	E	T	N	A	I	G	S	C	L	-	L	K	R	P	Y	L	K	N	D	N	T	A	K	V	A	49
hMPV 001	22	I	S	F	S	E	T	N	A	I	G	S	C	L	-	L	K	R	P	Y	L	K	N	D	N	T	A	K	V	A	49

# BPIV3 Mutation T1711I

		T1711I																																										
bPIV3	1690	P	E	T	I	E	D	W	D	P	I	E	D	E	N	I	L	D	N	I	V	K	T	V	N	D	N	C	S	D	N	Q	K	R	N	K	S	S	Y	F	W	1729		
hPIV3	1690	P	E	V	I	D	D	W	D	P	I	E	D	E	N	M	L	D	D	N	I	V	K	T	I	N	D	N	C	C	N	K	D	N	K	G	N	K	I	N	N	F	W	1729
hPIV1	1690	P	E	V	L	E	D	W	D	P	I	D	A	S	M	L	L	D	D	N	I	T	A	E	V	Q	N	N	I	P	-	-	L	K	N	E	R	T	P	F	W	1727		
hRSV A2	1744	P	L	L	S	N	K	K	L	I	K	S	S	A	M	I	R	T	Q	V	I	S	K	Q	L	Y	N	L	-	-	-	-	-	-	-	-	-	-	-	-	F	P	1772	
hMPV 83	1608	P	M	V	N	-	-	-	-	-	-	-	-	-	-	L	T	Q	V	I	D	P	T	Q	L	D	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	P	1626
hMPV 001	1608	P	M	V	N	-	-	-	-	-	-	-	-	-	-	L	T	Q	V	I	D	P	T	Q	L	D	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	P	1626

Fig. 26F

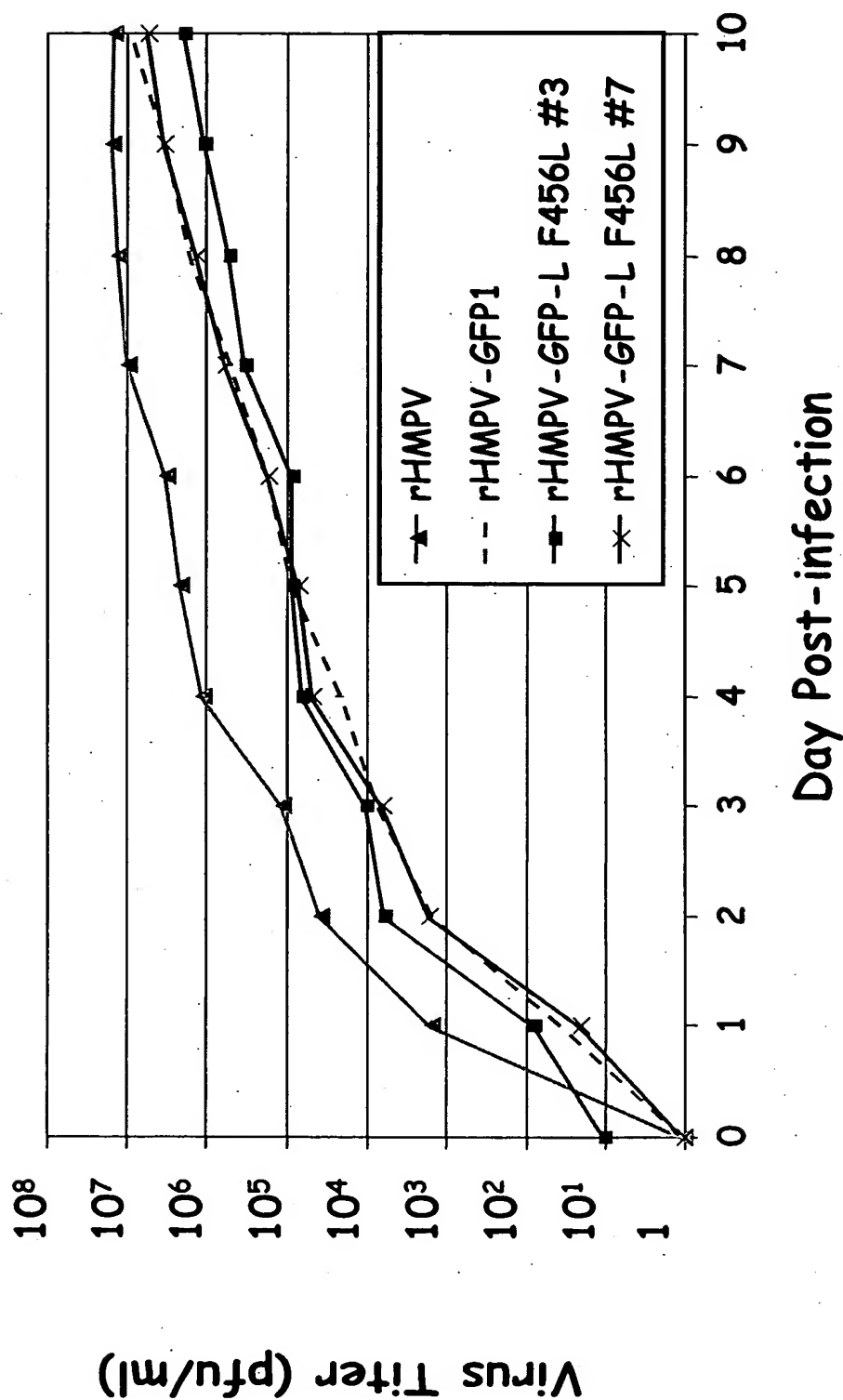


Fig. 27

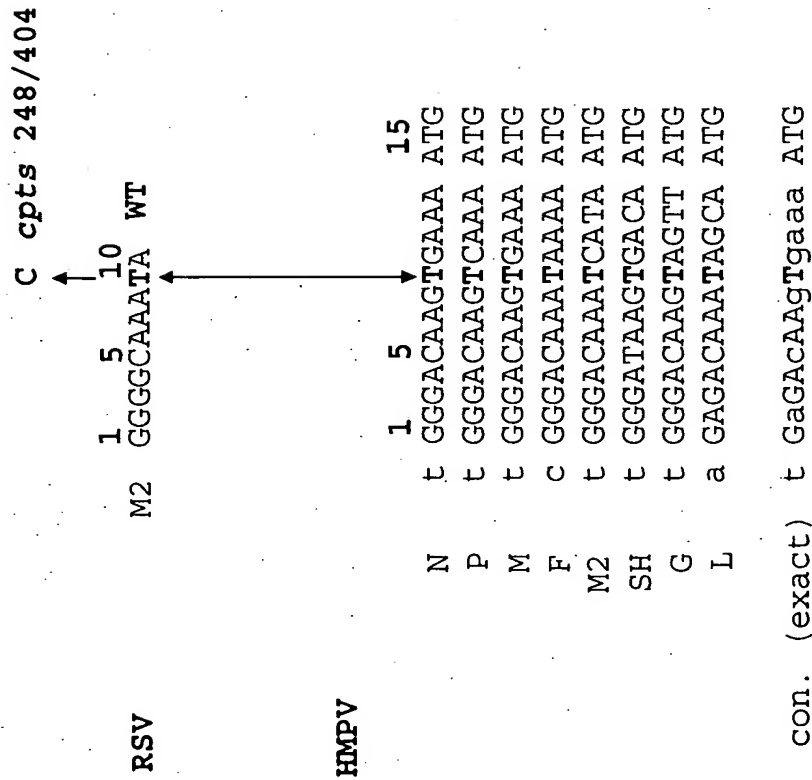
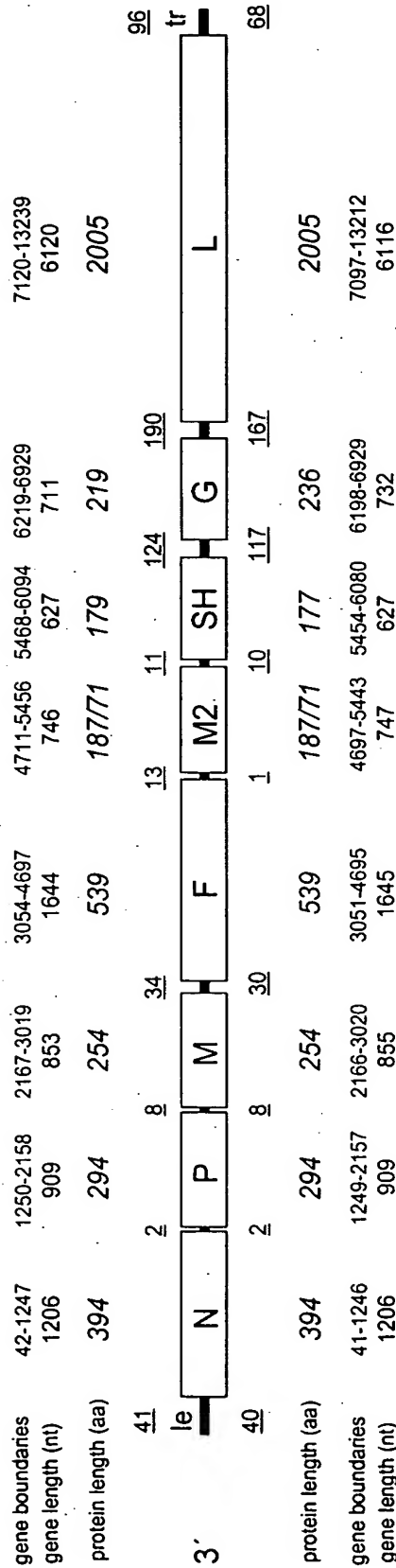


Fig. 28

**CAN97-83, 13,335 nucleotides**



**CAN98-75, 13,280 nucleotides**

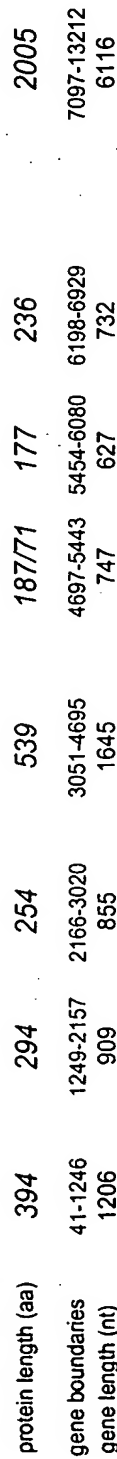


Fig. 29

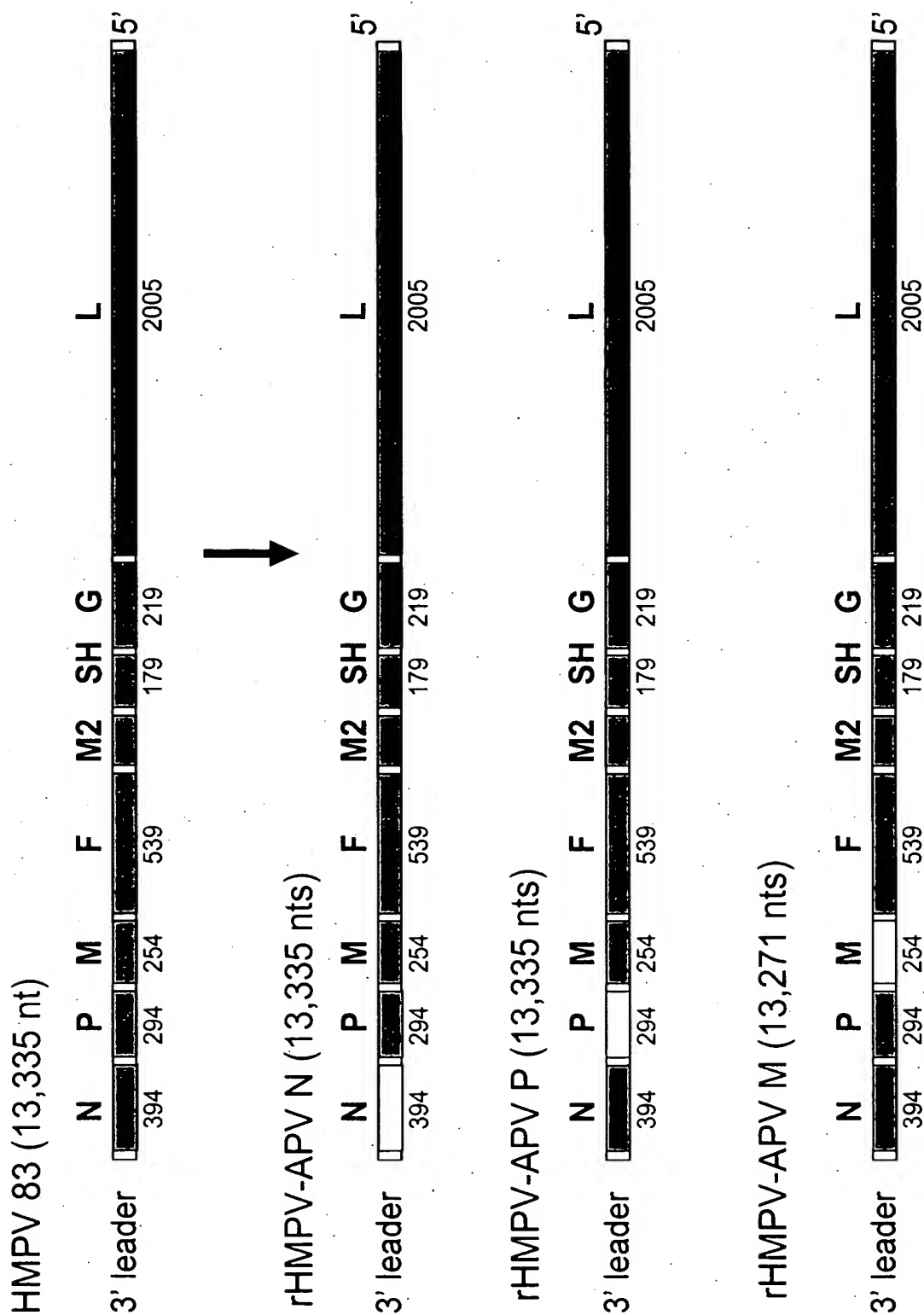


Fig. 30A



	gene-end	intergenic	gene-start
	1 13		1 16
le (83)	aattagTTTcaataAAAAAacat		GGGACAAgTgAAATGtctct N (83)
(75)	aattaaATTccaaACAAAAc-		GGGACAAaTaAAATGtctct (75)
N (83)	ttatgAGTAaAttAAAAA--	gt	GGGACAAgTcAAATGtctct P (83)
(75)	ttatgAGTAaAttAAAAA--	ct	GGGACAAgTcAAATGtctct (75)
P (83)	tatgtAGTTTtaataAAAAA--	taaaaaat	GGGACAAgTgAAATGgagtc M (83)
(75)	catgtAGTTTtaataAAAAA--	taaacaat	GGGACAAgTcAAATGgagtc (75)
M (83)	atTTTTAGTTATatatAAAAA--	tcaag- 24 nt-agaac	GGGACAAaTaAAATGtctctg F (83)
(75)	attatAGTTATatatAAAAA--	tttag- 20 nt-aaagc	GGGACAAgTgAAATGtctctg (75)
F (83)	cagttAGTTAattAAAAA--	taaaataaaaattt	GGGACAAaTcATAAATGtctcg M2 (83)
(75)	tagttAGTTAattAAAAA--	t	GGGACAAaTcATcATGtctcg (75)
M2 (83)	acttaAGTTAGtaAAAAA--	cacatcagagt	GGGACAAgTgACAAATGataac SH (83)
(75)	acttaAGTTAGtaAAAAA--	taaatagaat	GGGACAAaTgACAAATGataac (75)
SH (83)	agttttAGTTAattttAAAAA--	tattt-114 nt-aatat	GGGACAAgTagttATGgaggt G (83)
(75)	agtctAGTTAattttAAAAA--	ctcta-107 nt-aaaat	GGGACAAgTggccATGgaagc (75)
G (83)	aaattAGTTAacaaAAAAA--	tacga-180 nt-tccaa	GAGACAAaTagcAAATGgatcc L (83)
(75)	caagtAGTTAacaaAAAAA--	ctata-157 nt-ttcaa	GGGACAAaTaacAAATGgatcc (75)
L (83)	atgatAGTTAattAAAAA--	ttaaa-91 nt	tr (83)
(75)	ccattAGTTAattAAAAA--	ttata-63 nt	(75)
consensus	AGTTAnnnAAAAA		GGGACAAAnTnnnAAATG

Fig. 31



Percent amino acid or nucleotide sequence identity between the indicated strains of HMPV or RSV for the indicated proteins and ORFs

Viruses compared	percent amino acid sequence identity for indicated protein (percent nucleotide sequence identity for indicated ORF)								
	N	P	M	F	M2-1	M2-2	SH	G	L
CAN97-83 vs CAN98-75	96 (84)	85 (81)	97 (85)	95 (84)	96 (85)	89 (87)	59 (69)	37 (59)	94 (84)
CAN97-83 vs 00-1	99 (94)	95 (92)	99 (94)	98 (94)	98 (94)	96 (95)	85 (88)	70 (77)	99 (95)
RSV A2 vs RSV B1	95 (85)	90 (85)	91 (85)	89 (81)	91 (84)	61 (69)	72 (77)	55 (67)	92 (85)

CAN98-75	163	RPH T W HYL-----	177
CAN97-83	162	ECHCIYTIEWKCYHHSID----	179
00-1	162	VK YPT ETQS	183

# B. G protein

CAN98-75	1	AR	F	KM	IRS	HR	T	S	AP	M	TL	DHA	54
CAN97-83	1	MEVKVENIR	RAIDML	KARVKNR	VARSKCFK	NASL	ILIGIT	TL	S	I	A	L	NIYLI
00-1	1	T					V					K	54
		**	*****	***	****	***	***	***	*	****	***		
CAN98-75	55	TS	NMTKV	CVNM	V	PS	KTPMT	AAD	NTK	P	QA	LT	DS
CAN97-83	55	IQKTSS	SESEHHT	SSPPTES	KNKEAST	ISTD	NPDP	INPNS	QHP	TQQ	STEN	PTLN	PAA
00-1	55	M	NT	S	M	SR	TP	VP	S	T	SSP	GS	YF
		*	*	*	*	*	*	*	*	*	*	*	*
CAN98-75	109	LEDHLH	GTTP	A	VSQQT	EH	TLLRSTNRQ	TQ	TAEKKP	TRATTKET	1	62	
CAN97-83	109	SVPSE	TEPAST	PD	TNRLSS	VDRSTA	QPSERTK	TKPTV	HTRNNP	STASSTQS	1	62	
00-1	109	A	SP	T	PPF	TH	TP	A	S	A	K	R	S
		*	***	*	*	*	*	*	*	*	*	*	*
CAN98-75	163	TT	T	ST	ATQTLN	TNTQ	TSNG	EA	AR	RNNA	SSDQ	TQ	ADPS
CAN97-83	163	PPRATTKA	IRRA	TFRMS	STGKR	-PTT	SVQSD	SS	TTTQ	NHEETG	SANPQASVS	215	
00-1	163	RTA	T	L	T	R	-S	A	P	I	A	HKN	ASP
		*	*	*	*	*	*	*	*	*	*	*	*
CAN98-75	217	QHTQK	STTTTH	NTD	TSSPSS	-	236						
CAN97-83	216	TMQN	-----	-----	-----	-----	219						
00-1	216	TRIQRKS	VEANT	STTYNQTS	236								

Fig. 33B

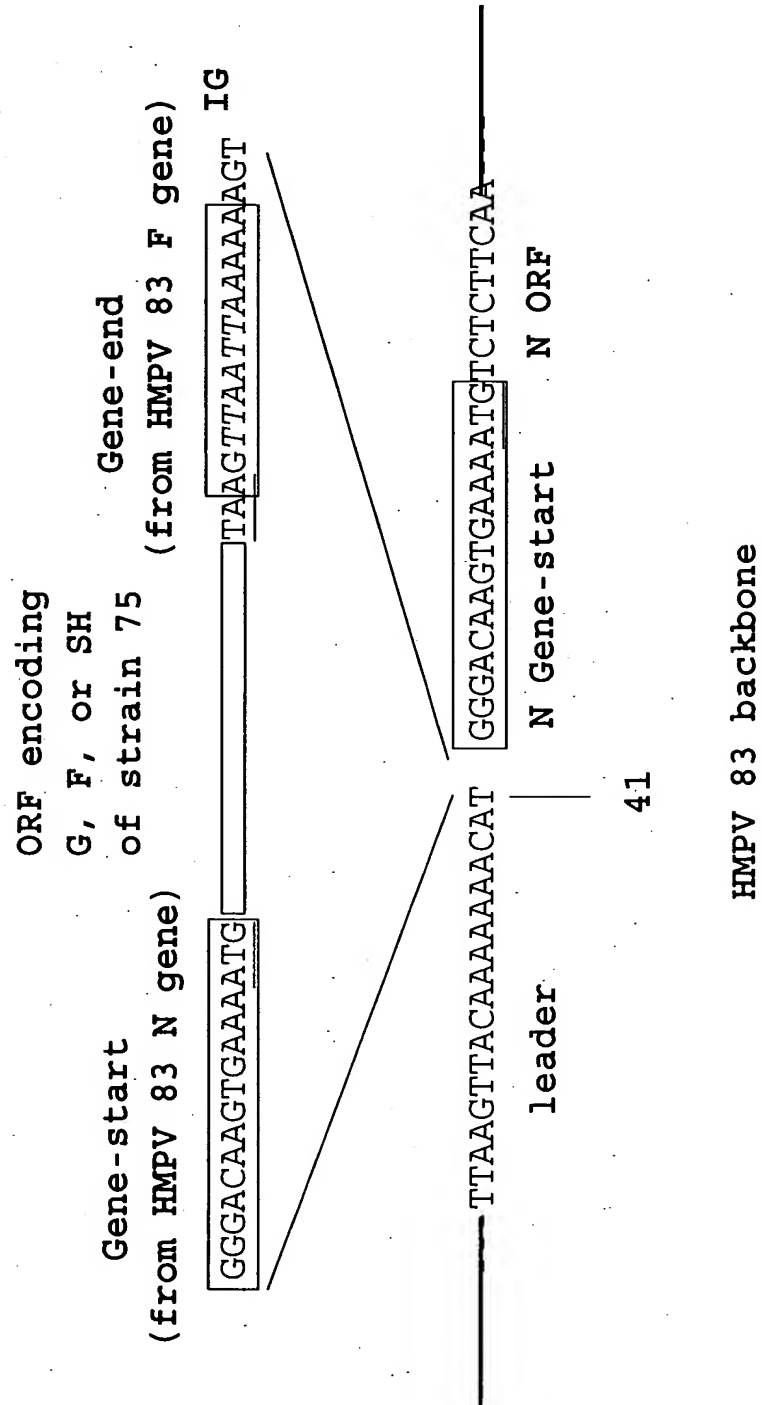


Fig. 34

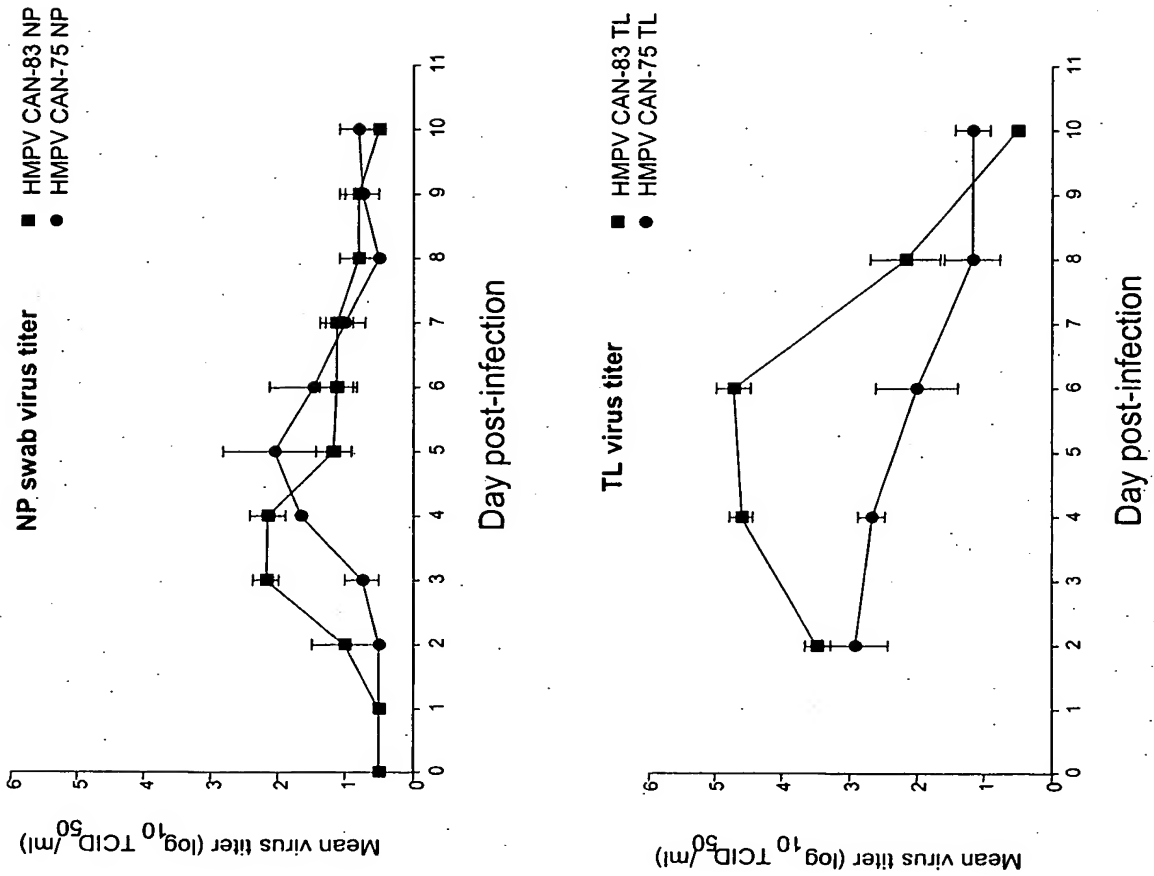
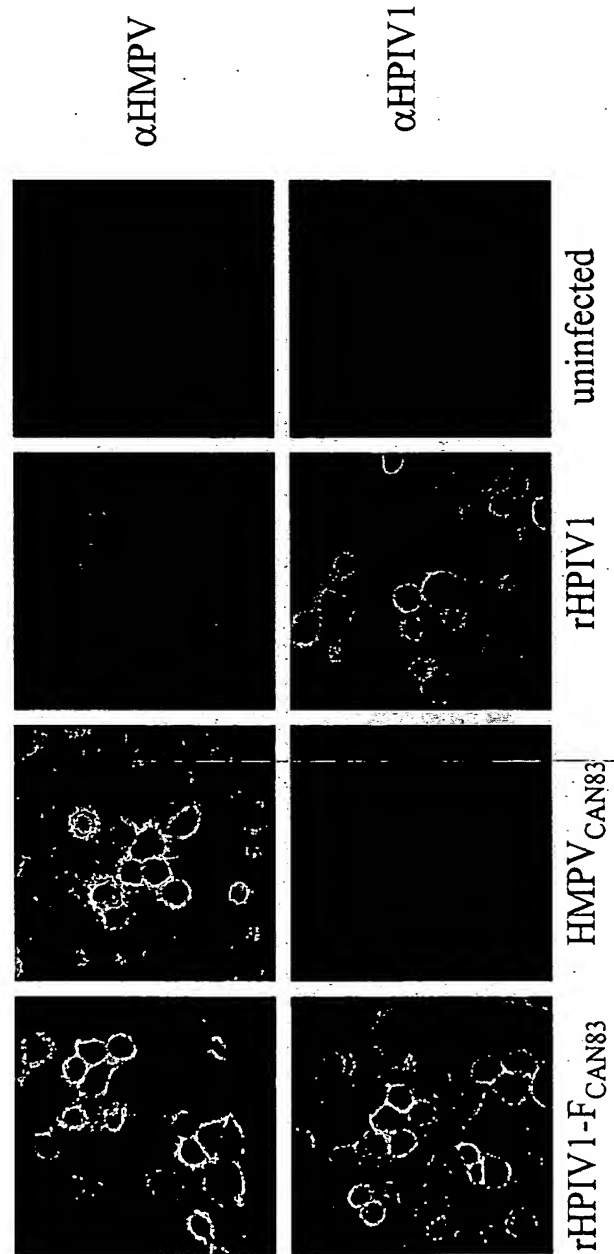
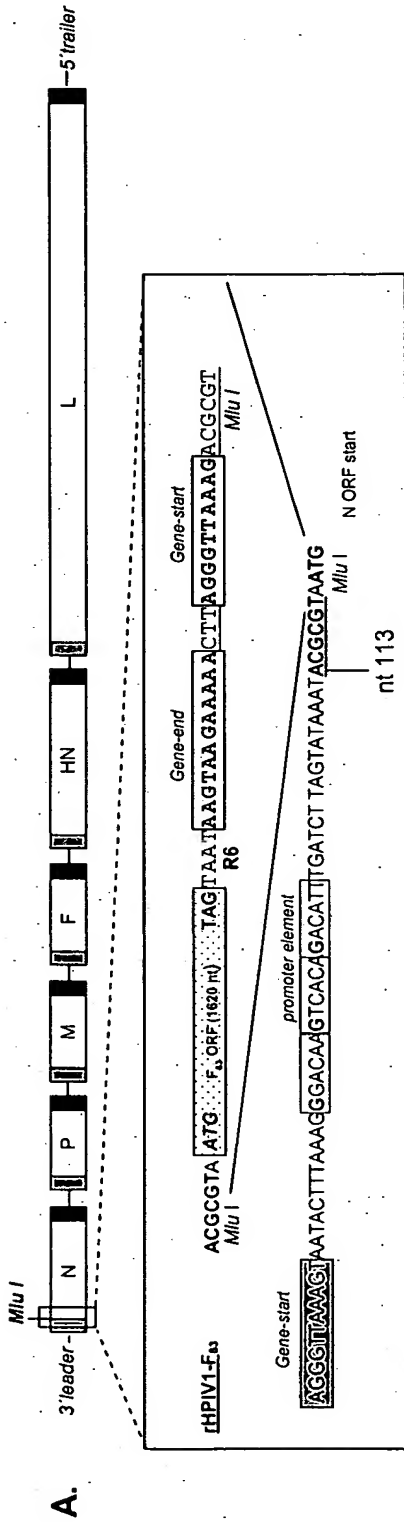


Fig. 35



**Fig. 36A & B**

HMPV strain 83

	10	20	30	40	50	60	70	80	90	100
1	ACGCGAAAA	AACGGGTATA	AATTAAGTTA	CAAAAAAACA	TGGGACAAGT	GAATAATGCT	CTTCAAGGGA	TTCACTGAG	TGATCTATCA	TACAAGCATG
101	CTATATATAA	AGAGTCTCAG	TATACAATAA	AGAGATATGT	AGGCAACAAC	ACAGCATGGA	CACCTCATC	ATTGCAACAA	GAATTAACAC	TATGTGTGG
201	AGAAATTTCTA	TATGCTAAGC	ATGCTGATTA	CAATATATGT	GCAGAAATAG	GAATACATAA	TATTAGCAC	CTCTAGGAT	CAGAGAGAT	ACAGCAGAT
301	CTAAGAAACT	CAGGCAGTGA	AGTCCAAGTG	GTTTTAACCA	GAACGTAATC	CTTGGGAAA	GTTAAAAACA	ACAAAGGAGA	AGATTTACAG	ATGTTAGACA
401	TACACGGAGT	AGAGAAAGC	TGGGTGGAAG	AGATAGACAA	AGAAGCAAGA	AAAAACATGG	CAACTTTGCT	TAAAGAATCA	TCAGGCAATA	TTCCACAAAA
501	TCAGAGGCCCT	TCAGCACCAG	ACACACCTAT	AATCTTATTA	TGTGTAGGTG	CCTTAATATT	TACCAAACTA	GCATCAACTA	TAGAAGTGGG	ATTAGAGACC
601	ACAGTCAGAA	GAGCTAACCG	TGTACTAAGT	GATGCACTCA	AAAGATACCC	TAGGATGGAC	ATACCAAAAA	TCGCTAGATC	TTTTCTATGAT	TTATTTGAAC
701	AAAAAGTGTA	TTACAGAAAT	TTGTTCAATTG	AGTATGGCAA	AGCATTAGGC	TCATCTCTCA	CAGGCAGCAA	AGCAGAAAAT	TTATTCCTTA	ATATATTCAT
801	GCAAGTTTAC	GGTGTGCTC	TAACAATGCT	GAGTGGGGA	GTCAATTGCCA	GGTCATCTAA	CAATATAATG	TTAGGACATG	TATCTGTCCA	AGCTGAGTTA
901	AAACAAGTCA	CAGAAGTCTA	TGACCTGGTG	CGAGAAATGG	CCCTGAATC	TGGGCTCTTA	CAATTAAGGC	AAAGCCCAA	AGCTGGACTG	TTATCACTAG
1001	CAAAATGTCC	CAACTTTGCA	AGTGTGTGTC	TCGGCAATGC	CTCAGGCTTA	GGCATAATAG	GTATGTATCG	CGGAGAGATG	CCAAACACAG	AACTATTTTC
1101	AGCAGCAGAA	AGCTATGCCA	AGAGTTTGAA	AGAAAGCAAT	AAAAATTAAT	TTTCTTCATT	AGGACTCACA	GATGAAGAAA	AAAGAGTATC	AGAACACTTT
1201	CTAATGTGTA	GTGACGACAG	TCAAAATGAT	TATGAGTAAT	TAAAAAAGTG	GGACAAGTCA	AAATGTCAAT	CCCTGAAGGA	AAAGATATTC	TTTTCATGG
1301	TAATGAAGCG	GCAAAATGG	CAGAAGCTTT	CCAAAAATCA	TTAGAAAAAC	CTAGTCTATA	AGATCTCAA	TCTATTATAG	GAGAAAAAGT	GAACACTGTA
1401	TCTGAACAT	TGGAATTACC	TACTATCAGT	AGACTTACCA	AACCGACCAT	ATTGTACAG	CCGAAGTTAG	CATGGACAGA	CAAAGGTGGG	GCAATCAAAA
1501	CTGAAGCAAA	GCAACAATC	AAAGTTATGG	ATCCTATTGA	AGAAGAAGAG	TTTACTGAGA	AAAGGGTGT	GCCCTCCAGT	GATGGGAAA	CTCCTGCAGA
1601	AAAGAGTTG	AAACCATCAA	CCAATCTAA	AAAGAGGTC	TCATTTCAC	CAAAATGAAC	AGGAAAAATAC	ACAAGTTGG	AGAAAGATGC	TCTAGACTTG
1701	CTTTCAAGTA	ATGAAGAGA	AGATGCAGAA	TCCTCAATCT	TAACCTTCGA	AGAAAGAGAT	ATTCTATCAT	TAAGCATTTA	AGCCAGACTA	GAATCGATTG
1801	AGGAGAAAT	AAGCATGATA	TTAGGGCTAT	TAAAGACACT	CAACATTGCT	ACAGCAGAT	CCACAGCAG	ACAGATGGG	ATCAGAGATG	CAATGATTGG
1901	CATAGGGGAG	GAACATATAG	CAGACATAT	AAAGAGACC	AAGGGAAAAG	CAGCAGAAAT	GATGGAAGAA	GAATGAACC	ACGGGACAAA	AATAGGAAC
2001	GGTAGTGTA	AATTAAGTGA	AAAGGCAAG	GAGCTCAACA	AAATTTCTGA	AGACGAGAG	ACAAGTGTG	AATCCGAAGA	AGAAGAAGAA	CTAAAGACAA
2101	CACAGGAAA	TAATCAAGAA	GATGACATTT	ACGAGTTAT	TATGTAGTTT	AATAAATAA	AAAAATGGA	CAAGTGAATA	TGGAGTCTTA	TCTGGTAGAC
2201	ACCTATCAAG	GCATCCCTTA	CACAGCAGT	GTTCAGTTG	ATCTAGTAGA	AAAGGACCTG	TTACCTGCNA	GCCTTAACAAT	ATGTTCCCC	CTGTTTCAGG
2301	CCAATACACC	ACCAGCAGTT	CTGCTTGATC	AGCTAAAGAC	TCTGACTATA	ACTACTCTGT	ATGCTGCATC	ACAAAAGTGT	CCAATACTAA	AAAGTGAATC
2401	ATCGGCCAG	GGTGCAGCAA	TGTCTGTACT	TCCCAAAAAAG	TTTGAAGTCA	ATGCGACTGT	AGCAGCTTGA	GAATATAGCA	AATTAGAATT	TGACAAACTT
2501	ACAGTCTGTG	AAGTAAAAAC	AGTTTACTTA	ACAAACATGA	AACCATATGG	GATGGTATCA	AGTTTGTGA	GCTCGGCCAA	ACCAGTTGGC	AAAAAAACAC
2601	ATGATCTAAT	CGCATTTATG	GATTTTATGG	ATCTAGAAA	GAACACACCA	GTTACATATC	CAGCATTTAT	CAATCAGTT	TCTATCAAGG	AGAGTGAATC
2701	AGCCACTGTT	GAAGCTGCAA	TAAGCAGTGA	AGCAGACCAA	GCTCTAACAC	AAGCCAAAAT	TGCACCTTAT	GCGGAGCTGA	TCATGATTAT	GACCATGAAC
2801	AATCCCAAAG	GCATATTCAA	GAAGCTTGA	GCTGGGACCC	AAGTTATAGT	AGAACTAGGA	GCATATGTCC	AGGCTGAAAG	CATAAGTAAA	ATATGCAAGA
2901	CTTGAGGCCA	TCAAGGAACA	AGATATGTGC	TGAAGTCCAG	ATAACAGCCA	AGCAACTGTA	CCAAAGAACTA	CCAACTCTAT	TCTATAGACT	AAAAAGTCGC
3001	CATTTTAGTT	ATATAAAAT	CAAGTTAGAA	TAAGAAATTAA	ATCAATCAAG	AACGGGACAA	ATAAAAATGT	CTTGGAAAAGT	GGTGATCAT	TTTTCAATGC
3101	TAATAAACACC	TCAACACGGT	CTTAAAGAGA	GCTACCTAGA	AGAAATCATGT	AGCACTATAA	CTGAGGGATA	TCTTAGTGT	CTGAGGACAG	GTTGGTATAC
3201	CAACGTTTTT	ACATTAGAGG	TGGGTGATGT	ATGAAACCTT	ACATGTTCTG	ATGGACCTAG	CCTAATAAAA	ACAGAAATTAG	ATCTGACCAA	AAGTGCACTA
3301	AGAGCTCTCA	AAACAGTCTC	TGCTGACCAA	TTGGCAAGAG	AGGAACAAT	TGAGAAATCCC	CCAAAGAACTA	GGTTGTTCT	AGGAGCAATA	GCATCGGTG
3401	TTGCAACAGC	AGCTGCAGTC	ACAGCAGGTG	TTGCAATTGC	CAAAACCAT	CGGCTTGAGA	GTGAAGCTAC	AGCAATTAAG	AATGCCCTCA	AGACGCCCAA
3501	TGAAGCAGTA	TCTACATTTG	GGAATGGAGT	TCGAGTGTG	GCAACTGCAG	TGAGAGAGCT	GAAAGACTTT	GTGACCAAGA	ATTTAACTCG	TTCAATCAAC
3601	AAAAACAAGT	GCGACATTTA	TGACCTAATA	ATGGCCGTTA	GCCTCAGTCA	ATTCACAGTA	AGGTTCTTAA	ATGTTGTGCG	GCAATTTTCA	GACAATGCTG
3701	GAATAACACC	AGCAATATCT	TTGGACTTAA	TGACAGATGC	TGAACATAGCC	AGGCCCGTTT	CTAACATGCC	GACATCTGCA	GGACAAATAA	AATTGATGTT

Fig. 37A

HMPV strain 83 (continued)

```
3801 GGAGAACCGT GCGATGGTGC GAAGAAAGGG GTTCGGAATC CTGATAGGGG TCTACGGGAG CTCGGTAATT TACATGGTGC AGCTGCCAAT CTTTGGCGTT 3900
3901 ATAGACACGC CTTGCTGGAT AGTAAAAGCA GCCCTTCTT GTTCCGGAAC TCTTAAGAGC AGACCAAGGG TGGTATTGTC 4000
4001 AGAATGCAGG GTCAACTGTT TACTACCCAA ATGAGAAAG CTGTGAAGAA AGAGGAGACC ATGCTCTTTG CGACACAGCA GCGGAATTA GTTGTGCTG 4100
4101 GCAATCAAGG GAGTGCACA TCAACATATC CACTACAAAT TACCCATGCA AAGTCAGCAC AGGTAAGACAT CCTATCAGTA TGGTTGCACT GTCTCTCTT 4200
4201 GGGGCTCTGG TTGCTTGCTA CAAAGGAGTA AGCTGTTCCTA TTGGCGACAA CAGAGTAGGG ATCATCAAGC AGCTGAACAA GGGTTGCTCC TATATAACCA 4300
4301 ACCAAGATGC AGACACAGTG ACATAGACA ACATGTGATA TCAGCTAAGC AAAGTTGAGG GTGAACAGCA TGTATATAAA GGCAGACCAG TGTCAAGCAG 4400
4401 CTTTGATCCA ATCAAGTTTC CTGAAGATCA ATTCATGTT GCACCTGACC AAGTTTTTGA GAACATTGAA AACAGCCAGG CCTTGGTGA TCAATCAAA 4500
4501 AGAATCCTAA GCAGTGACA GAAAGGGAAT ACTGGCTTCA TCAATGTAAT AATTCTAATT GCTGTCTTGG GCTCTAGCAT GATCCTAGTG AGCATCTTCA 4600
4601 TTATATCAA GAAACAAAG AAACCAACGG GAGCACTCC AGAGCTGAGT GGTGTCAAA ACAATGGCTT CATACACAC AGTTAGTTAA TTAATAATAA 4700
4701 AATAAATTT GGGACAATC ATATGTCTC GCAAGCTCC ATGCAATAT TAATGCAGG GCAATGCAA CAGAGAAAGT GAGTGAAGT GAGTGAAGT TTAACCAAA 4800
4801 TTAGTGAGT TGGCCAGATA GATACTTAT ATTAAGATCA AACTATCTAT TAAATCAGCT TTTAAGGAAC ACTGATAGAG CTGATGGCCT ATCAATAATA 4900
4901 TCAGGCGCAG GCAGAGAGA CAGAACGCAA GATTTGTTC TAGGTTCCAC CAATGTGTT CAAGTTATA TTGATGATA CCAAGCATTA ACAAAGCTA ACAAAGCTG 5000
5001 CAGCTGTCTA CAGTCTACAC AACATAATCA AGCACTACA AGAAGTTGAA GTTAGGCAAG CTAGAGATAG CAAACTATCT GACAGCAAGC ATGTGGCACT 5100
5101 CCATRAACTTA ATCTTATCTT ACATGGAGAT GAGCAAACT CCCGCATCTT TAATCAACAA TCTCAAAAGA CTGCCGAGAG AAAAATGAA AAAATTAGCA 5200
5201 AAGCTGATAA TTGACTTATC AGCAGGCGCT GACATGACT CTTTATATGC CCTGCAAGC AGTGAAGCA TTAATCAAGT GCAGTGAGCA TGGTCTCTG 5300
5301 TTCAATTAATA TAGAGGTGA TGAATGATA TGGACTCAA AAGAATTAAA AGAAGCTTGG TCCGATGGG TAGTGAAGTC TCACACCAAC ATTACAAT 5400
5401 GTTAATTAGA AAACATAGAA ATTATATATG TCAAGGCTTA CTTAAGTTAG TAAAAACACA TCAGAGTGGG ATAAGTGACA ATGATACAT TAGATGTCT 5500
5501 TAAAGATGAT GGGTCTTCAA AAACATGTAC TCACCTCAA AAATATCA AAGACCATC TGGTAAAGTG CTTATGTCAG TTAAGTTAAT ATTAGCTTTA 5600
5601 CATCAATTT TCACAATAAC AATCACTATA ATTTACATAA AAGTAGAAA CAATCTACAA ATATGCCAGT CAAAACACTA CTCAGACAA GAGACTCAC 5700
5701 CATCAATATC CACATCCGTC ACAACCAAGA CCACCTAGA CCATGATATA ACACAGTATT TTTAAAAGATT AATTCAAAGG TATACAGATT GTGTAATAA 5800
5801 CAAGSACACA TGCTGAAAA TAAGCAGAAA TCAATGCACA AATATAACAA CATATAATT TTTATGCTTT AAACCTGAGG ACTCAAAAT CAACAGTTGT 5900
5901 GATAGACTGA CAGATCTATG CAGAAACAAA TCAAAATCAG CAGCTGAAGC ATATCTACA ATATGCCAGT CAAAACACTA CTCAGACAA GAGACTCAC 5700
6001 ATCACCACAT AATAGATTAA ACCCAATCTT GAATGTTAAA ACTAGACTAG GATCCGCTCA AGACTATCAG TTAATATGTT TAGTTATTTT AAAATATTG 6100
6101 AGAATAGGTA AGTTTCTATG GCATTTCTA GCAATAGGTA ATAATTAA GCTTAATTAT AATTAAACA TTAATTTAAA TCGTAATCTAT TTAATTTACA 6200
6201 AGTAAAAAC AAAATATGG GACAAGTAGT TATGGAGGTG AAAGTAGAGA ACATTCGAGC AATAGACATG CTCAAAGCAA GAGTGAATAA TCGTGTGGCA 6300
6301 CGTAGCAAT GCTTTAAAA TGCTTCTTTA ATCCTCATAG GAATTAATAC ACTGAGTATA GCTCTCAATA TCTATCTGAT CATAACTAC ACAATACAA 6400
6401 AACCTCATC TGAATCAGAA CACCACACCA GCTCACACC CACAGRATCC AACAGGAAG CTTCAACAAAT CTCACAGAC ACCCAGACA TCAATCCAA 6500
6501 CTCACAGCAT CCAACTCAAC AGTCCACAGA AAACCCACA CTCAACCCCG CAGCATCAGT GAGCCCATCA GAACAGAAC CAGCATCAAC ACCAGACACA 6600
6601 ACAACCCGCC TGCTCTCGT AGACAGGTCC ACAGCACAA CAAAGTGAAG GCCACCACTT TCCGCTAGAG CAGCAGAGA AAAAGACCAA CCACACCATC 6800
6701 CTTCCAGTAC ACAATCCCA CCACGGGCAA CAATCATGAA GAAACAGGTT CAGCGAACC ACAGGCATCT GTAGACAAA TGCAAACTA GCACACCAAC 6900
6801 AGTCCAGTCC GACAGCAGCA CCACAACCCA AAATCATAGC TCTAAAGTAA AACATGTAGG TACCAACAAAT CAAGAACCA AACAGCACT CACAATCTCC 7000
6901 AATATAAAC CAAATTAGTT AACAAAAAAT ACGAGATAGC TCTAAAGTAA AACTTTTGGC CACATCTAAA CAACATACA ACCATCTCAA GAAAGAAAAC 7100
7001 CTAACACAGC AACGACACCA TGTCAGCTTT GTCTCAATCT CTCTGGAGA TCCACTGTTA ATGCTATCT CCCTGATTCG TACCTTAAAG GAGTAATTTT 7200
7101 TGGGAAAAAC AGCATCCAAG AGACAATAG CAAATGAGTA AGACCTACT TAAAAATGA CAACTGCA GAACACTGCA AAAGTTGCCA TAGAGATCC TGTATTGAG 7300
7201 TTTTGTGAA ACTAATGCA TTGGTTTCATG TCTCTTAAA AGACCTACT TAAAGTAGTA GAGCCAGTGA ATATGCAACA TGAAATAATG AAGATGTAC 7400
7301 CATGTGAGC TCAAAATGTC AGTCAATCT AAAATGAAA TATCAGTAA CAAGTAGTA GAGCCAGTGA ATATGATGT GATTGGCTG AATTAAGTAC 7500
7401 ACAGTTGTGA GCTCACA TTTAAACAGT TTTTAAACAG GAGTAAAAAC ATTAGCACTC TCAAAATTGAA TATGATATGT GATTGGCTG GATTGGCTG 7600
7501 TACATCAGAT GATACCTCAA TCCTAAGTTT CATAGATGTA GAATTTATAC CTAGTTGGGT AAGCAACTGG TTTAGTAATT TTTTATTGT ATCATCATAT GGATGTATG 7700
7601 ATTTTGAAT TCAGAGAGA GGAAGTAATA AGAACCGGT CAATCTTATG CAGGTCAATG GGTAAATTAG TTTTATTGT TTTTATTGT 7800
7701 TCAAGAGCAA CAAAGGCAA AGAGTGAGCT TCTTCACATA CAATCAACTG TTAACATGGA AAGATGTGAT GTTAAGTAGA TTTAATGCGA ATTTTGTAT 7800
```

Fig. 37B



HMPV strain 83 (continued)

7801 ATGGGTAAGC AATAGTCTGA ATGAAAGATCA GGAAGGGCTA GGGTTGAGAA  
7901 ATGCTAAGCT TATGTTGCAA TGAAGGTTTC TCACCTGTGA AAGAGTTGGA  
8001 GTACTAGATT TAGAAATACT TTATTGAATG GATTAACATA TCAATTAAACA  
8101 TAATGATATT CCAATGTATG AAGTTGTACT TAAATTATTA GGAGATACTT  
8201 TTATACTATA TATTCAGAAAT TTTTGGTCAAT CCAATGGTAG ATGAAGAGAGA  
8301 TGGAGAGCTT GACAGAACTA AGAGGGGCAT TCATATTAAG GATTATCAAA  
8401 GCTTAGCAAA AGATGGACTA TGTACTTCAA AGCTAAAAAT TACCCAGTCC  
8501 GAACAAGAGT TTTCTGTCTC TGAATAAACCC AATCTTGAGA TGGTATTAAA  
8601 AGAATTACTT ACCTGAGACG ATAAAAAATC GATATTTAGA AGAACTTTTC  
8701 AGATTAATAA TTTGATCAAA AGGAACCTTA AGTTTATGTA GTTAGACAAG  
8801 GAATTAAAGT TAGGTAGAAAT GTTGTCTATG CAACCAAGGA AACAGCGACA  
8901 TCCCGGAAC CTTAACAAAG TATGGTGATC TAGATCTTCA GAGAAATATG  
9001 TAATAATTAC ATTGCAAGAG CATCCATAGT AACGATTTG AGCAAGTTCA  
9101 GAATTACATG GAACACAAAG CTTATTCTGT TGGTTACATC TTATCGTTCC  
9201 GTGAATATGA TATAGATAAG ATAGAAGAGC AAGTGGTCT ATATAGATAT  
9301 TATATCTTTA TTGGATGTTG TATCTGTAAA GACACGGTGT CAAATGACAT  
9401 TTATCTGAAG GTTTAGATGA AGTGAAGGCA GATTATCGT TAGCAGTAAA  
9501 AAGAGGGGCA AACATATATA TCAAGGGATC TTCAGTTTAT AAGCAGGTG  
9601 AGTAGAGGCA TGGATAAACA CAATATTAGA TGACATTAAA ACTAGTGTG  
9701 ATAGTTAGTC TGATATTAAAG AAATCTCTGG CTGTATAACT TATACATGCA  
9801 ATAAACATT AACATCAGTG CAGAGATTTT TTGAAATTA AAGGAAAAAT  
9901 TCCAGTAGTC TTCTATAGAT CTTTCTATAG AAGACCCCTT GATTTTTAA  
10001 AAAATGAAA CGAAGTAAG TTTCTTCAA GCCTTACTAT CAATAGAAA  
10101 GATCAGAACG ACAAGCAAAA GTAACAAGTG ACATCAATAG AACAGCAGTT  
10201 ACATACAGC AGAAATGAAG AAGAAGTGGG AATCATGCA GAAAAATAA  
10301 CACAAAGCTG AAAAAGTTGT AAACATGATA TCAGGGCAA AATCTATAAC  
10401 CTGTATCTAT GATGTTGGAG AATCTAGGAT TATTATCTAG AATATTGTC  
10501 ATGTTGTCAA ATCTCTAGGA CTTTAAGAGA GACATCATGG AATAATATG  
10601 TATGCAACTA GTTCTCATTT GAAAGGGATA ATTATAGAAA AGTTCAAGC  
10701 CGAGTACTCA AGAGAAAAA TTAGTACCTG TTTATAACAG ACAATTTCT  
10801 GTATAAAGG ACACAGGCT TGGCAGGATT ACTCAACAAG ATCTGTCTTG  
10901 ATGAGTGTA ATTTCTTACA TAGATTATCT GTCAGTAGTA GACCTATGGA  
11001 CTAGTCCCTAT TAATCAAGCA CTAAGTGAGA GATTTGGGAA TGAAGATATT  
11101 AATAGACAA TTAACAGGTA GAAGCCCAA ACAGTTAGT TTAATACCCC  
11201 AGTTATAAAT TAGTAGATAA GATAACTTCT GATCAACATA TCTTTTCC  
11301 AAGGTCAGAA AACGATCAG TTTCTAAATA AGAGAAAAA TTATTTCCAT  
11401 TGGGATATTA ACAGAACAAAT GCATAGAAA TAAATTTTTC AAGAAGACT  
11501 CTATGTGTCT TTAATACTAA ACTTTTATGT AGTTGGGGAT CTCAGGGGAA  
11601 GGATTGACAA TACTTTTGG AGAATGTTCA GCAAGTTAT GTTTGAACCA  
11701 AGGCTACATA GGGTTTAAAG ACTGGTTTAT AGACAGTTG AGATCAGCTG  
GTAATCTGCA AGGTATGTTA ACTAATAAAC TATATGAAC TGTAGATTAT 7900  
AGGTTTATTT ATGATGAGA TCCTTAGGAT TACTGAACAT GCTCAATTCA 8000  
AAATTAATAA ATAAAAACAG ACTCAGAGTT CATAGTACCG TACTAGAAA 8100  
TGAGATGAT CAAATTATTA ATCAATAAAA ACTTAGAGAA TGTGACAGAA 8200  
TGCAATGGAT GCTGTCAAAT TAAACAATGA AATCAGAAA ATCTAAGGT 8300  
GGATTTGTGG ACAACAACA AAGTGGCCC AAAATTAAAA ACTTAAAAAGT 8400  
AACTCGAATT AAGTGAACAA GACTTTCTAG AGCTTGCTGC AATACAAATT 8500  
TGACAAAAGC ATATCACCTC CTAAAGATT AATATGGTCT GTGTATCCAA 8600  
AATGCGAGTG ATAGTCTCAA AACAGAAGA GTACTAGT ACTATTTTAA 8700  
AATATTTAAA CGATAAGGAG CACTATGTCT CATTAACTGG AAAAGAAAAG 8800  
AATACAAATA TTGGCAGAAA AATTGTTAGC TGATAACATT GTACCTTTCT 8900  
GAAATCAAAT CAGAACCTTC TTCTATCAA ACCAGAAGAA ATGATAGTTA 9000  
ACCAAGCCTT TAGATATGAA ACTACAGCGA TCTGTGCGA TGTAGCAGAC 9100  
TATGACTACA ATGATATGTG CCTATAGACA TGCACCACA GAAACAAAAG 9200  
CACATGGCG GTATTGAAG ATGGTGTCAA AAATCTGGA CAATGGAAGC 9300  
CTTTATTAAA CGTGACAAAC CAATCAATAG ATGTAAGTAA ACCAGTCAAG 9400  
AATGCTAAAA GAAATAAGAG ATGCATACAG AAATATAGGC CATAACTTAA 9500  
ATTCAATCTG AAGGATGAT CATCTTACC CCTATAAAA AGCTTTGAG 9600  
AGTCAATAGG GAGTCTATGT CAAGAATTAG AATTAGGGG AGAAACATA 9700  
TGAATCAAAG CAACATCTCT TGGCAGGAA ACAGTTATT AAACAACATA 9800  
GAGGTAGTAG ATCTATGGAT GAACATACCA ATGCAATTTG GAGGAGGAGA 9900  
CTGAGGCAAT CAGCCATGTA GATATCTGT TAAAAATATC AGTAAACATA 10000  
AAATGAAGCT GCTACACTGA CAACACTAAT GAGAGATCT CAAGCTGTG 10100  
ACCAGTATCT TAAGTCTTTC CCCAAATCAA CTTTTCAGTG ATAGTGTAT 10200  
CACCTGTTTA TCCTCATGG CTGAGAGTAT TATATGAATC ATTGCCCTTT 10300  
CAACTTATTA CAGAGAACAT CCGCTATTAA TGGTGAAGAT ATGACAGGG 10400  
GTAGTTGTTG ATAGTATAGA AATCCAATC AATCTAATG GTAGGTGAT 10500  
AAATAGTTGG AGTAACTCT CCTAGCATCA CTACATGAT GAGTGTCTA 10600  
TGACAGAACT ACAAGGGGTC AAAGAGGTC AAAAGCCCT TGGGTAGGT 10700  
TCAAAACAAC AAGAGAAACA GCTAGAAACA ATTGAAAAA TGAGATGGT 10800  
GGAGTTTAGG CATTAGCTAC AATGTGTAA AACCTTATT ACCTAGTTT 10900  
ATTCAGCA TCAAGTCCAG CTTATAGAAC AACAAATTAC CATTCGACA 11000  
AATTTGGTCT TCCAAAATGC AATCAGCTGT GGAATTAGCA TAATGAGTGT 11100  
AATTGAAGA AATPAGACAT ATGCCACCAC CAGTGTTC AAGGAAATTC 11200  
GGACAAAATA TATTGTGTA CACTAGGGA AATGCTCATG CCCACTATTA 11300  
GGAAACAATC TTTATGAGTC TTTTATGAGCA GCATTGACAT GTCATTGGT 11400  
GGGTGACGG GTTTATATCA GATCATGCTT TTATGGACT CAAAATATTC 11500  
AAACATTAAA GATGAAGATA TAGTAGATGA ATCAATAGAT AAATTTGTTA 11600  
AAGGTTAAGA AAGGATTAAT GTTATATGAT GTAAATTC TATCACTAGT 11700  
AATTGCATGA AATACCTTGG ATTGTCAATG CCGAAGGTGA TTTGGTTGAG 11800

Fig. 37C

HMPV strain 83 (continued)

11801	ATCAAGTCAA	TTAAATCTA	TTTGCAACTG	ATAGAACAAA	GCTTATTTTT	AAGAATAAAT	GTTTTGAAC	ATACAGATAT	GGCACATGCT	CTCACACGAT	11900
11901	TAATCAGAAA	GAAGTTAATG	TGTGATAATG	CACGTTAAC	CCCAATTTC	TCCCCAATGG	TTAACCTTAAC	TCAAGTTAT	GATCCCAAA	CACAATTAGA	12000
12001	TTACTTCCCC	AAGATAACAT	TCGAAAGGCT	AAAAAATTAT	GACACAAGTT	CAAAATTATGC	TAAAGGGAAG	CTAACAGAA	ATTACATGAT	ACTATTGCCA	12100
12101	TGGCAGCATG	TTAATAGATA	TAACTTTTGC	TTTAGTTCTA	CTGGATGTAA	AGTTAGTCTG	AAAACATGTA	TTGGAAAACT	TATGAAAGAC	CTAAATCCTA	12200
12201	AAGTTTGTGA	CTTTATTGGA	GAAGGAGCAG	GAAATTGGAT	GGCCAGAACAA	GCATGTGAAT	ATCCTGATAT	TAAATTGTGA	TATAGAAATC	TGAAAGATGA	12300
12301	CCTTGATCAT	CATTATCCTC	TGGAATACCA	GAGAGTGATA	GGTGAATTAA	GCAGAAATCAT	AGATAGTGGT	GAAGCACTTT	CAATGGAAC	AAACAGACGA	12400
12401	ACTCAAAAAA	CTCATTTGGA	TTTGATACAC	AGGGTAAGCA	AAGATGCTTT	ATTAATAAAT	TTATGTGATG	CAGAATTAA	GGACAGAGAT	GATTTTTTTA	12500
12501	AGATGGTAAT	TCTATGGAGA	AAACATGTAT	TATCATGCAG	AATTTGCACT	ACTTATGGGA	CGGACCTCTA	TTTTATTGCA	AAGTATCATG	CTAAAAGACTG	12600
12601	CAATGTAAAA	TTACCTTTTT	TTGTGAGATC	AGTTGCTACT	TTCAATTATGC	AGGGTAGTAA	GCTGTCAAGT	TCAGAAATGCT	ACATACTCTT	AACACTAGGC	12700
12701	CACCACAACA	GTTTACCTTG	CCATGGAGAA	ATACAAAATT	CTAAGATGAA	AATAGCAGTG	TGTAATGATT	TTTATGCTGC	AAAAAACTC	GACAAATAAT	12800
12801	CAATTGAAGC	TAATTGTAAA	TCACCTTTTGT	CAGGCTAAG	AATACCTATA	AATAAGAAGG	AACTAGATAG	ACAGAGAAGA	TTATTAAAC	TACAAAGCAA	12900
12901	TCATTCTTCT	GTAGCAACAG	TTGGCGGTAG	CAAGATCATA	GAGTCTAAGT	GGTTAACAAA	CAAAGCAAAGT	ACAATAATTG	ATTGGTTAGA	ACATATTTTA	13000
13001	AATTCTCCAA	AGGGCGAATT	AAATTATGAT	TTTTTTGAAG	CATTGGAGAA	CACCTTACCCT	AAATATGATT	AACTAATAGA	TAACTTAGGG	AAATGCAGAG	13100
13101	TTAAAAAACT	GATCAAGATA	ACAGGATACA	TGCTTGTAAG	TAAAAAATGA	AAAATGATGA	AGATGACAAA	ATAGATGACA	ACTTCATACT	ATTCTAAATT	13200
13201	AATTATTTGA	TTATGCAATT	ATATGATAGT	TAAITAAAAT	TAAAAAATTAA	AAATCAAAAAG	TTAAAAATTTA	AAACCTATCA	TTAAGTTTAT	TAAAAATAAG	13300
13301	AAATTTATAAT	TGAATGTATA	CGGTTTTTTT	GCCGT							13335
	10	20	30	40	50	60	70	80	90	100	

Fig. 37D

rHMPV-GFP

	10	20	30	40	50	60	70	80	90	100
1	ACGCGAAAAA	AACGCGTATA	AATTAAGTTA	CAAAAAACA	TGGACAAGT	GAAAAATGTG	AGCAAGGGCG	AGGAGCTGTT	CACCGGGGTG	GTGCCCATCC
101	TGGTGGAGCT	GGACGGCGAC	GTAACCGGC	ACAAGTTCA	CGTGTCCGGC	GAGGCGGAGG	GGCATGGCAAG	CTAGCCCTGA	AGTTTCATCTG	200
201	CACACCGGCG	AAGCTGCCCC	TGCCCTGGCC	CACCTCGTGG	ACCACCTTGA	CCTACGGCGT	GGAGTGGCTTC	AGCCGTACC	CGACACATC	300
301	GACTTCTTCA	AGTCCGCCAT	GCCGGAAGGC	TACGTCCAGG	ACGCGACCAT	CTTCTTCAAG	GACGACGGCA	ACTACAAGC	CCGCGCCGAG	400
401	AGGGCGACAC	CCTGGTGAAC	CGCATCGAGC	TGAAGGGCAT	CGACTTCAAG	GAGGACGGCA	ACATCCTGGG	GCACAAGCTG	GAGTACAACT	500
501	CAACGTCTAT	ATCATGGCGG	ACAAGCAGAA	GAACGGCATC	AAGTGAAT	TCAAGATCCG	CCACAACATC	GAGGACGGCA	CGGTGCAGCT	600
601	TACCAGCAGA	ACACCCCAT	CGGGACCGG	CCCGTCTGTC	TGCCCGACAA	CCACTACCTG	AGCACCCAGT	CGCCCTGAG	CAAGACCCC	700
701	CGCATCACAT	GGTCTGCTG	GAGTTCGTGA	CCGCGCCCGG	GATCACTCTC	GGCATGGACG	AGCTGTACAA	GTAAGTTAAT	TAAAAAAGTG	800
801	AAATGTCTCT	TCAAGGGATT	CACCTGAGTG	ATCTATCAT	CAAGCATGCT	ATATTAAAG	AGTCTCAGTA	TACATAAAG	AGAGATGTAG	900
901	AGCAGTGACA	CCCTCATCAT	TGCAACAAGA	AATACACTA	TTGTGTGGAG	AAATTTATTA	GCTTAAGCAT	GCTGATTACA	AATATGCTGC	1000
1001	ATACATATA	TAGCACAGC	TCTAGGATCA	GAGAGAGTAC	AGCAGATTCT	AAGAAATCTA	GGCAGTGAAG	TCCAAGTGGT	TTTAACCCAGA	1100
1101	TGGGGAAGT	TAAAAACAAC	AAAGGAGAAG	ATTTACAGAT	GTTAGACATA	CACGGAGTAG	AGAAAAGCTG	GGTGAAGAG	ATAGACAAAG	1200
1201	AACAATGGCA	ACTTTGCTTA	AAGAATCATC	AGGCAATATT	CCACAATACT	AGTCAGAA	GCTAACCCGTG	TACTAAGTGA	TGCACCTCAA	1300
1301	TTAATATTTA	CCAACTAGC	ATCAACTATA	GAAGTGGGAT	TAGAGACCAC	AAAGTGTAAT	ACAGAAATTT	GTTCAATTGAG	TATGGCAAG	1400
1401	GGATGGACAT	ACCAAAATC	GCTAGATCTT	TCTATGATTT	ATTTGACAAA	AAGCTTACGG	TGCTGGTCAA	ACAATGCTGA	GGTGGGAGT	1500
1501	ATCCTCTACA	GGCAGCAAAG	CAGAAAGTTT	ATTCGTAAAT	ATATTCAATG	AAGCTTACGG	GAAGTCTATG	ACCTGGTGGG	AGAAATGGGC	1600
1601	TCATCTAACA	ATATAATGTT	AGGACATGTA	TCTGTCCAAG	CTGAGTTAAA	ACAAGTCACA	GAAGTCTATG	ACCTGGTGGG	AGAAATGGGC	1700
1701	GGCTCTAGCA	TTTAAGGCAA	AGCCCAAAAG	CTGACAGTGT	ATCATTTGAC	AATTGTCCCA	CTTTTGCAG	TGTTTCTC	GGCAATGCCT	1800
1801	CATAATAGAT	ATGATCGCG	GGAGAGTGCC	AAACAGTGA	CTATTTTACG	CAGCAGAAAG	CTATTGCCAG	AGTTTGAAG	AGAACTATA	1900
1901	TCTTCATTAG	GACTCAGCA	TGAAGAAAAA	GAGGTGTCAG	AACACTTTCT	AAATGTGAGT	GACGACAGCT	AAAATGATTA	TGAGTAATTA	2000
2001	ACAAGTCAAA	ATGTCTATCC	CTGAAGGAAA	AGATATTCTT	TTTATGGGTA	ATGAAGCGGC	AAAATTTGCA	GAAGCTTTCC	AAAAATCAT	2100
2101	AGTCAATAAA	GATCTCAATC	TATTATAGGA	GAATAAGTGA	ACACTGTATC	TGAACATTTG	GAATTACCTA	CTATCAGTAG	ACCTACCAA	2200
2201	TGTCAGAGCC	GAAGTTAGCA	TGGACAGACA	AAGTGGGGC	AATCAAACT	GAAGCAAAAG	AAACAATCAA	AGTTATGGAT	CCTATTGAAG	2300
2301	TACTGAGAAA	AGGGTGCTGC	CCTCCAGTGA	TGGGAAAACT	CCTGCAGAAA	AGAAAGTTGAA	ACCATCAACC	AATACTAAA	AGAAGTCTC	2400
2401	AATGAACCCAG	GAATAATACAC	AAAGTTGGAG	AAAGATGCTC	TAGACTTGCT	TTCAGACAAAT	GAAGAAGAAG	ATGACAGATC	CTCAATCTTA	2500
2501	AAAGAGATAC	TTCATCATTA	AGCATTTGAAG	CCAGACTAGA	ATCGATTGAG	GAGAAATTA	GCATGATATT	AGGGCTATTA	AGAACACTCA	2600
2601	AGCAGGACCC	ACAGCAGCAA	GAGATGGGAT	CAGAGATGCA	ATGATTGGCA	TAAGGGAGGA	ACTAATAGCA	GACATAATA	AGAGGCCAA	2700
2701	GCAGAAATGA	TGGAAGAAGA	AATGAACCCAG	CGGACAAAAA	TAGGAAACGG	TAGTGTAAA	TTAACTGAAA	AGGCAAGGA	GCTCAACAA	2800
2801	ACGAGAGCAC	AAGTGGTGA	TCCGAAGAG	AAGAAGAACT	AAAAGACACA	CAGGAAATA	ATCAAGAAAG	TGACATTTAC	CAGTTAATTA	2900
2901	TAAAAATAAA	AAATGGGACA	AGTGAAAATG	GAGTCTATC	TGTTAGACAC	CTATCAAGGC	ATCCCTTACA	CAGCAGCTGT	TCAAGTTGAT	3000
3001	AGGACTGTT	ACCTGCAAGC	CTAACAAAT	GGTTCCCCCT	GTTTCAGGCC	AATACACCAC	CAGCAGTTCT	GCTTGATCAG	CTAAAGACTC	3100
3101	TACTCTGTAT	GCTGCATCAC	AAAGTGTCTC	AATACTAAA	GTGAATGCAT	CGGCCCAAGG	TGCAGCAATG	TCTGTACTTC	CCAAAAGTT	3200
3201	CGGACTGTAG	CACCTTGACGA	ATATAGCAAA	TTAGAAATTT	ACAACTTAC	AGTCTGTGAA	GTAATAACAG	TTTTACTTAAC	AACCATGAAA	3300
3301	TGATATCAAA	GTTTGTGAGC	TCGGCCAAAC	CAGTTGGCAA	AAAAACACAT	GCATTAATCG	CAATTGCGA	TTTTTATGGAT	CTAGAAAAGA	3400
3401	TACATAACCA	GACTTTATCA	AATCAGTTTC	TATCAAGGAG	AGTGAATCAG	CCACTGTGGA	ATATTCAATA	AGCATTGAGG	GAGCCAAGC	3500
3501	GCCAAAATTG	CACCTTATGC	GGGACTGATC	ATGATTATGA	CCATGAACAA	TCCCAAGGC	ATATTCAATA	AGCTTGGAG	TGGACCCAA	3600
3601	AACTAGGAGC	ATATGTCCAG	GCTGAAGCA	TAAGTAAAT	ATGCAAGACT	TGGAGCCCAT	AAGGAACAAAG	ATATGTGCTG	AAGTCCAGAT	3700
3701	CAACCTGACC	AAGAACTACC	AACTCTATTC	TATAGACTAA	AAAGTCGCCA	TTTTAGTTAT	ATAAAAATCA	AGTTAGATA	AGAAATGCTAG	3800

Fig. 38A

rHMPV-GFP (continued)

3801 CGGACAAAT AAAAATGTCT TGGAAAGTGG TGATCAATTT TTCAATGCTA  
3901 CACTATAACT GAGGATATC TTAGTGTCTT GAGGACAGGT TGGTATACCA  
4001 GGACCTAGCC TAATAAAAC AGAATTAGAT CTGACCAAAA GTGCACATAAG  
4101 AGAATCCCGC ACAATCTAGG TTGTGTTCTAG GAGCAATAGC ACTCGGTGT  
4201 GCTTGAGAGT GAAGTCACAG CAATTAAGAA TGCCCTCAAA ACAGCCAATG  
4301 AGAGAGCTGA AAGACTTTGT GAGCAAGAA TTAACCTCGT CAATCAACAA  
4401 TCAACAGAAG GTTCTCTAAAT GTTGTGCGG AATTTTCAGA CAATGCTGGA  
4501 GGCCGTTCT AACATGCCGA CATCTGCAGG ACAATAAAA TTGATGTTGG  
4601 TACGGAGCT CCGTAATTTA CATGGTGCAG CTGCCAATTT TTGGCTGTAT  
4701 AGGGAACCTA TGCTTGCTTC TTAAGAGAG ACCAAGGTTG GTATTGTCAG  
4801 AGGAGACCAT GTCTTTTGGG ACACAGCAGG GGGAAATTAAT GTTGTGTCAG  
4901 GTCAGCACAG GAAGACATCC TATCAGTATG GTTGCACTGT CTCTCTTGG  
5001 GAGTAGGGAT CATCAAGCAG CTGAACAAGG GTTGCTCTTA TATAACCAAC  
5101 AGTTGAGGGT GAACAGCATG TTATAAAGG CAGACCAGTG TCAAGCAGCT  
5201 GTTTTGTGAG ACATTGAAA CAGCCAGGCC TTGCTAGATC AATCAACAG  
5301 TTCTAATTGC TGCTCTTGGG TCTAGCATGA TCCTAGTGAG CATCTTCATT  
5401 TGTCACAAAC AATGGCTTCA TACCACACAG TTAGTAAAT AAAAATAAAA  
5501 ATGCGGGGCT AAATGCAAC GAGGAAGTGA GTTAAGTTT AACCAAAAT  
5601 AATCAGCTTT TAAGGAACAC TGATAGAGCT GATGGCTAT CAATAATAT  
5701 ATGTGTTTCA AGTTATATT GATGATAACC AAAGCTAAC AAAAGCTGCA  
5801 TAGGAGGGCT AGAGATAGCA AACTATCTGA CAGCAAGCAT GTGGCACTCC  
5901 ATCAACAATC TCAAAAGACT GCGGAGAGAA AAATGAAA AAATTAGCAA  
6001 TGCAAGACAG TGAAAGCATT AATCAAGTGC AGTGAGCATG GTCTGTTTT  
6101 AAGCTTTGTC CGATGGGATA GTGAAGTCTC ACACCAACAT TTACAATGT  
6201 AAAACATC AGAGTGGAT AAGTGACAA TATTGCACTT AGTTAATAT TAGCTTTACT  
6301 GACCAATCTG GTAAAGTGT TATTGCACTT AAGTTAATAT TAGCTTTACT  
6401 ATCTACAAAT ATGCCAGTCA AAAAATGAA TACAGAAAGA AGACTCACCA  
6501 ACAGTATTTT AAAAGATTAA TTCAAAGGTA TACAGATTCT GTAATAAACA  
6601 TATAAATTTT TATGCTTTAA ACCTGAGGAC TCAAAAATCA ACAGTTGTGA  
6701 ATCATACAGT AGAATGCCAT TGCATATACA CAATTGAGTG GAAGTGCTAT  
6801 TCCGCTAAG ACTATCAGTT CAATAGTTTA GTTATTTTAA AATATTGAG  
6901 TTAATTATAA TTAAACATTT ATTTAAATC GTAACTATTT AATTTACAA  
7001 ATTCGAGCAA TAGACATGCT CAAGCAAGA GTGAAAAATC GTGTGCGACG  
7101 TGAGTATAGC TCTCAATATC TATCTGATCA TAACTACATC AATCAAAAA  
7201 CAAGTAAGCT TCAACAATCT CCACAGACAA GCATCAACAC CAGACACAAC  
7301 GCATCAGTGA GCCCATCAGA AACAGAAACA GTCCACACAA GAACAACCC  
7401 GAACAAGAC AAAACCGACA GTCCACACAA GAACAACCC AAGCACAGCT  
7501 CACCACTTTC GCGATGAGCA GCACAGGAAA AGACCAACC ACAACATCAG  
7601 GCGAATCCAC AGGCATCTGT AAGCACAATG CAAAACACTAGC ACACCAACA  
7701 CATGTAGGTA CCAACAATCA AGAAACCAAA AGAACAATCA CAATCTCCCT

Fig. 38B

rHMPV-GFP (continued)

7801 CTTTGGCCCA CATACTAACA ACATCAACAAC CATCTCAAGA AAAGAAACTG  
7901 CACTGTAAAT GTCTATCTCC CTGATTCGTA CCTTAAAGGA GTAAATTTCTT  
8001 AAAAATGACA ACACTGCAAA AGTTGCCATA GAGAACTCCTG TTATTGAGCA  
8101 AGGTAGTAGA GCCAGTAAAC ATGCAACATG AAATAATGAA GAATGTACAC  
8201 TAGCACTCTC AAATTGAATA TGATATGTGA TTGGCTGCAA TTAAAGTCTA  
8301 AGTTGGGTAA GCAACTGGTT TAGTAATTGG TACAACTCTCA ATAAGTTAAT  
8401 GGTCAATTGG TAAATTAGTT TTATTGTAT CATCATATGG ATGTATCGTC  
8501 AACATGGAAA GATGTGATGT TAAGTAGATT TAATGCGAAT TTTTGTATAT  
8601 AATCTGCAAG GTATGTTAAC TAATAAACTA TTGAAACTG TAGATTATAT  
8701 GTTTTATTAT GAGTGAGATC CTTAGGATTA TAGTAACATG TCAATTCAAT  
8801 ATTTAAATAAT AAAAACAGAC TCAGAGTTCA TAGTACCGTA TTAGAAATA  
8901 AGATGTATCA AATTATTAAT CAATAAAAC TTAGAGAAATG CTGCAGAATT  
9001 CAATGGATGC TGTCAAAATTA AACAAATGAA TCACAAAAT CCTAAGGTTG  
9101 ATTTGTGGAC AACAAACAAA GGTGGCCCAA AATTAAAAAC TTAAAGTGC  
9201 CTCGAATTAA GTGAACRAAG CTTTCTAGAG CTTGCTGCAA TACAATTGA  
9301 ACAAGCCAT ATCACCTCCT AAAAGATTAA TATGGTCTGT GTATCCAAAG  
9401 TGCAGGTAT AGTCTCAAAA CAAGAAGAT ACTAGAGTAC TATTTAAAG  
9501 TATTTAAACG ATAAGGACA CATTTGCTCA TTAAGTGAA AAGAAGAGA  
9601 TACAATAATT GGCAGAAAA TTGTTAGCTG ATACATTTGT ACCTTTCTTC  
9701 AATCAAAATCA GAACCTTCTT CTATCAAAAC CAGAAGAAAT GATAGTTATA  
9801 CAAGCCTTTA GATATGAAC TACAGCGATC TGTGCGGATG TAGCAGACGA  
9901 TGACTACAAT GATATGTGCC TATAGACATG CACCAACAGA AACAAAGGT  
10001 CATGGCGGT ATTGAAGAT GTGTCAAAA ACTCTGGACA ATGGAAGCTA  
10101 TTATTAAACG GTGACAACA ATCAATAGAT GTAGTAAAC CAGTCAAGTT  
10201 TGCTAAAGA AATAAGAT GCATACAGAA ATATFAGGCCA TAACTTAA  
10301 TCAATCTGAA GGAGTATGC ATCCTACCCC TATAAAAAG GTCTTGAGAG  
10401 TCAATFAGGA GTCTATGTCA AGAATTAGAA TTTAGGGGAG AAAGCATAAT  
10501 AATCAAAAGCA ACATCCTTTG GCAGGGAAC AGTTATTCAA ACAACTAAAT  
10601 GGTAGTAGAT CTATGGATGA ACATACCAAT GCAATTTGGA GGAGGAGATC  
10701 GAGGCAATCA GCCATGTAGA TATTTCTGTTA AAAATATCAG CTAACTAAA  
10801 ATGAACGTGC TACACTGACA ACACATAATGA GAGATCCTCA AGCTGTTGGA  
10901 CAGTATCTTA AGTCTTTCCC CAAATCAACT TTTCAGTGAT AGTGCTATAC  
11001 CTTGTTATC CTGATGGGCT GAGAGATTA TTGAATCAT TGCCTTTCA  
11101 ACTTATTACA GAGAACATCC GCTATTAATG GTGAAGATAT TGACGGGCT  
11201 AGTTGTTGAG TAACATCTCC TAGCATCTCA ATCTAATGGT AGCTGATAT  
11301 ATAGTTGAGG AAGGGTCAA AAGGCCCTTG GGTAGGGTCG  
11401 ACAGAACTAC AAGGGTCAA AAGAGCAGC TAGAAGCAAT TGGAAAAATG  
11501 AAAACAACAA AGAGACAGC TAGAAGCAAT TGGAAAAATG AGATGGGTGT  
11601 AGTTTAGGCA TTAGCTACAA ATGTGTAAAC CCTTTATTAC CTAGGTTTAT  
11701 TCCAGCATC AGTTCCAGCT TATAGAACAA CAAATTACCA TTTCACACT  
GGCAAAACAG CATCCAAGAG ACAATAGCA ATGGATCTCT TTAATGAATC 7900  
TTAGTGAAC TAATGCAAT GGTTCATGTC TCTTAAAAAG ACCCTACTTA 8000  
TGTGAGACTC AAAATGCGAG TCAATTCTAA AATGAAATA TCAGATTACA 8100  
AGTTGTGAGC TCACACTATT GAAACAGTTT TTAACAAGGA GTAAAAACAT 8200  
CATCAGATGA TACCTCAATC CTAAGTTTCA TAGATGTAGA ATTATACCT 8300  
TTTGGAAATC AGAAGAGAGG AAGTAATAAG AACCGTTCA ATCTTATGCA 8400  
AAGAGCAACA AAGCAAAAAG AGTGACTTC TTCACATACA ATCAACTGTT 8500  
GGGTAAGCAA TAGTCTGAAT GAAATCAGG AAGGCTAGG GTTGAGAAGT 8600  
GCTAAGCTTA TGTGCAATG AAGGTTCTC ACTTGAAA GAGTCGAAG 8700  
ACTAGATTA GAATACTTT ATTGAATGGA TTAACAGATC AATTAACAAA 8800  
ATGATTATCC AATGTATGAA GTTGTACTTA AATTATTAGG AGATACTTTG 8900  
ATACTATATA TTCAGAAATT TTGTCATCC AATGTTAGT AAGAGAGATG 9000  
GAGAGCTTGA CAGAACTAAG AGGCGATTC ATATTAGGA TTATCAAAAG 9100  
TTAGCAAAAG ATGACTATG TACTTCAAAG CTAAAATTA CCCAGTCAA 9200  
ACAAGAGTTT TCTGTTCTCG AAAAACCAA TCTTGAGATG GTATTAAATG 9300  
AATTACTTAC CTGAGACGAT AAAAAATCGA TATTTAGAG AACTTTCAA 9400  
ATAATAAAT TGATCAAAAG GAACCTAAA GTTATGTAGT TAGCAAGAA 9500  
ATTAAGTGA TTGTAATGTA TGTGTATGTA ACCAGGAAA GACGACAAA 9600  
CCGGAACCT TTAACAAGTA TGGTGATCTA GATCTTCAAG GAATAATGGA 9700  
ATAATACAT TGCAAGAGCA TCCATAGTAA CAGATTTGAG CAGTTCAAC 9800  
ATTACATGGA ACACAAAGCT TATTTCTGTT GTTACATCTT ATCGTTCTTA 9900  
GAATATGATA TAGATAAGAT AGAAGAGCAA AGTGTCTAT ATAGATATCA 10000  
TATCTTTATT GGATGTTGTA TCTGTAAAGA CAGGTGTCA AATGACATCT 10100  
ATCTGAAGT TTAGATGAAG TGAAGGCGA TTATCGCTTA GCAGTAAAA 10200  
GAAGGGAAA CATATATATC AAGGATCTT CAGTTTATAA GCAAGGTGAT 10300  
TAGGACCATG GATAAACACA ATATTAGAT ACATTAAAC TAGTGTGAG 10400  
AGTTAGTCTG ATATTAGAA ACTTCTGGCT GTATACTTA TACATGCATG 10500  
AAAACATTA CATCAGTGCA GAGATTTTTT GAAATTTAAA GGGAAAATGA 10600  
CAGTAGCTT CTATAGATCT TTCTATAGAA GGACCCCTGA TTTTAACT 10700  
AAATGAACG AAAGTAAAT TCTTCAAAGC CTTACTATCA ATAGAAAAA 10800  
TCAGAACGAC AAGCAAAAGT AACAGTGAC ATCAATAGAA CAGCAGTTAC 10900  
ACTACAGCAG AAATGAAGAA GAAGTGGAA TCATTGCGA AACATAACA 11000  
CAAGCTGAA AAGTTGTAA ACATGATATC AGGACAAAA TCTATAACCA 11100  
GTATCTATGA TGTGGAGAA TTAGGATTA TTATCTAGAA TATTTCACT 11200  
TTTGTCAAAT CTCTAGGACT TTAAGAGAGA CATCATGAA TAATATGAA 11300  
TGCAACTAGT TCTCATTTGA AAGGATAAT TATAGAAAG TTCAGCATG 11400  
AGTACTCAAG AGAAAAAAT AGTACCTGTT TATAACAGC AATTTCTCTC 11500  
ATAAAGGAC ACCAGGCTTG CGACGATTAC TCAACAAGAT CTGTCTTGG 11600  
GAGTGTAAAT TTCTTACATA GATTATCTGT CAGTAGAGA CCTATGGAAT 11700  
AGTCCCTATTA ATCAAGCACT AAGTGAGAGA TTTGGGAATG AAGATATTAA 11800

Fig. 38C





HMPV strain 75

	10	20	30	40	50	60	70	80	90	100
1	ACGCGAAAA	AACGCGTATA	AATTAAATTC	CAAAACAAATC	GGGACAATA	AAAATGTCTC	TTCAAGGGAT	TCACCTAAAGT	GATCTGTCACT	ATAAACATGC
101	TATATTAAAA	GAGTCTCAAT	ACACAATATA	AAGAGATGTA	GGCACCAATA	CTGCAGTAC	ACCTTCATCA	TTGCAGCAAG	AGATAACACT	TTTGTGTGGA
201	GAGATTCTTT	ACACTAAACA	TACTGATTAC	AAATATGCTG	CAGAGATAGG	GATACAATAT	ATTTCACCGG	CTCTAGGATG	AGAAAGAGTA	CAACAGATT
301	TAAGAAATTC	AGGCAGTGAA	GTTCAAGGTG	TTCTAACCAA	GACATACTCT	TTAGGGAAAG	GTAAAAATAG	TAAAGGGGAA	GAGTTGCAAA	TGTTAGATAT
401	ACATGAGGTG	GAAAAGAGTT	GGGTAGAAGA	AATAGACAAA	GAGGCAAGAA	AAACAATGGT	GACTTTGCTA	AAGGAATCAT	CAGGTAACAT	CCACAAAAAC
501	CAGAGGCCTT	CAGCACCCAGA	CACACCAATA	ATTTTATTAT	GTGTAGGTGC	TTTAATATTC	ACTAAACTAG	CATCAACAAT	AGAAAGTTGA	CTAGAGACTA
601	CAGTTAGAG	AGCTAACAGA	GTGCTAAGTG	ATGCCTCAA	AAGATACCTT	AGGGTAGATA	TACCGAAGAT	TGCTAGATCT	TTCTATGAAC	TATTTGAGCA
701	GAAGGTGAT	TACAGGAGTC	TATTCATTGA	GTATGGGAAA	GCTTTAGGCT	CATCTTCAAC	AGGAAGCAAA	GCAGAAAGTT	TGTTTGTAAT	TATATTTATG
801	CAAGCTTATG	GAGCCGGTCA	AACAATGCTA	AGGTGGGGTG	TCATTGGCAG	ATCATCTAAC	AACTAATATG	TAGGACATGT	GTCTGTGCAA	GCTGAATTGA
901	AGCAATTTAG	AGAGGTTTAT	GATTTGGTGA	AGGAATGGG	TCCTGAACTT	GGGCTTTTAC	ATCTAAGACA	AGTCCAAAG	GCAGGACTGT	TATCGTTGGC
1001	CAATTGCCCC	GATTTTGCTA	GTGTTGTTCT	TGGTAATGCT	TCAGGTCTAG	GTATAATCGG	AATGTACAGA	GGAAGAGTGC	CAACACAGAG	GCTATTTTCT
1101	GCAGCAGAAA	GTATATGCCAG	AAGCTTAAAA	GAAGCAACA	AAATCAACTT	CTCCTCATTA	GGGCTCACAG	ACGAAGAAA	AGAAGCTGCA	GAACACTTCT
1201	TAAACATGAG	TGATGACAA	CAAGATGATT	ATGAGTAATT	AAAAAATGG	GACAAGTCAA	AATGTCAATC	CCTGAAGGAA	AAGATATCCT	GTTCAATGGT
1301	AATGAGCAG	CAAAATAGC	AGAACTTTC	CAGAAATCAC	TAAAAGATC	AGGTCAACAA	AGAACCCAGT	CTATTGTAGG	GGAAAAGTA	AACACTATAT
1401	CAGAAACTCT	AGAGCTACCT	ACCATCAGCA	AACCTGCACG	ATCATCTACA	CTGCTAGAGC	CAAAATTTGG	ATGGGCAGAC	AGCAGCAGAG	CCACCAAAAC
1501	CACAGAAAA	CAACCAACCA	AAACAACAGA	TCCTGTTGAA	GAAGAGGAAC	TCAATGAAAA	GAAGATATCA	CTTCCAGTG	ATGGGAAGAC	TCCCGCAGAG
1601	AAAAATCAA	AATCTCAAC	CAATGTAAAA	AAGAAAGTTT	CCTTCACATC	AAATGAACCA	GGGAAATATA	CCAACTAGA	AAAAGATGCC	CTAGATTTCG
1701	TCTCAGACAA	TGAGGAGGAA	GAGGCAGAGT	CTCTCAACTT	AACCTTTGAA	GAGAGAGACA	CATCATCACT	AGCATTTGAG	TCAGAGATAG	AATCAATAGA
1801	AGAGAAGCTA	AGCATGATAT	TAGGACTGCT	TCCGTACACT	AGCATTTGCA	CAGCAGAGCC	AACGGCTGCA	AGAGATGGAA	TCAGAGATGC	AATGATTTGGT
1901	ATAAGAGAG	AACATAATAG	AGAAATATA	AAAGAAGCAA	AGGGAAGAC	AGCTGAAATG	ATGGAAGAGG	AAATGAATCA	AAGGTCAAAA	ATAGGTAATG
2001	GCAGTGTAAA	ACTAACCGAG	AAGGCAAAAG	AACTTAATAA	AATTGTTGAA	GACGAGAGCA	CAAGCGGTGA	ATCAGAAGAA	GAAGAAGAAC	CAAAAAGAAC
2101	TCAGGATAAC	AATCAAGGAG	AAGATATTTA	CCAGTTAATC	ATGTAGTTTA	ATAAAAATAA	ACAATGGGAC	AAGTCAAGAT	GGAGTCTAT	CTAGTGGACA
2201	CTTATCAAGG	CATTCCCTAC	ACAGCTGCTG	TTCAAGTTGA	TCTGGTAGAA	AAAGACTTAC	TACCAGCAAG	TTTGACAATA	TGGTTTCCTC	TATTTCCAAG
2301	CAACACACCA	CCAGCGGTTT	TGCTCGATCA	GCTAAAGACC	TTGACAATAA	CAACTCTGTA	TGCTGCATCA	CAGAAATGGT	CAATACTCAA	GGTAAATGCA
2401	TCAGTCCAGG	GTGCTGCTAT	GTCTGTACTT	CCCAAAAAAT	TCGAAGTAAA	TGCAACTGTG	GCATTTGATG	AATACAGCAA	ACTTGACTTT	GACAAGTTAA
2501	CGGTTTGGGA	TGTTAAACAA	GTTTATTTGA	CAACCATGAA	ACCATATGGG	ATGGTGTCAA	AATTTGTGAG	TTCAAGCCAA	TCAGTTGGCA	ACAAGACACA
2601	TGATCTAATT	GCACCTGTGT	ACTTCATGGA	CCTAGAGAAA	AATATACCTG	TGACATATCC	AGCATTCATA	AAGTCAGTTT	CAATCAAGA	GAGTGAGTCA
2701	GCCACTGTTG	AAGCTGCAAT	AAGCAGTGAG	GCCGACCAAG	CATTAAACACA	AGCCAAAATT	GCACCTTATG	CAGGACTAAT	CATGATCATG	ACCATGAACA
2801	ATCCAAAAGG	TATATTTCAAG	AAACTAGGAG	CTGGAACACA	AGTGATAGTA	GAGCTAGGGG	CATATGTTCA	AGCCGAGAGC	ATCAGCAGGA	TCTGCAAGAG
2901	CTGGAGTCAC	CAAGGAACAA	GATATGTACT	AAATCCAGA	TAAAATAAAC	TGTCCTAATC	AATAATTGCT	TATATAATCT	TAAAGATCAA	TGAGCTTAT
3001	ATTATAGTTA	TATAAAAAA	TTTAGAACTA	AGGAAGTATT	AATAGAAAGC	GGGACAAGTA	AAAATGTCTT	GGAAAGTGAT	GATTATCATT	TCGTTACTCA
3101	TAAACACCTCA	GCACGGACTA	AAGGAAAGTT	ATTTAGAAGA	ATCATGTAGT	ACTATAACTG	AAGGATATCT	CAGTGTTTTA	AGAACAGGTT	GGTACACCAA
3201	TGCTTTTACA	TTAGAAGTTG	GTGATGTTGA	AAATCTTACA	TGTACTGATG	GACCTAGCTT	AATCAAAAACA	GAACCTGACC	TAAACAAAAG	TGCTCTAAGA
3301	GAACCTCAAA	CAGTTTCTGC	TGATCAGTTA	CGAGAGAGAG	AACAATTGA	AAATCCAGA	CAATCAAGGT	TTGTCTTAGG	TGCAATFAGCT	CTTGGTGTG
3401	CCACAGCAGG	AGCAGTCAAC	GCAGGCATTG	CGATAGCCAA	AACCATAAGG	CTTGAGAGTG	AGTGAATGTC	ATCAAAAGT	GCTCTCAAAA	CAACCAATGA
3501	GGCAGTATCC	ACACTAGGAA	ATGGAGTGCG	AGTCTAGCC	ACCGCAGTAA	GAGAGCTGAA	AGAAATTTGTG	AGCAAAAACC	TGACTAGTGC	AATTAACAG
3601	AACAAATGTG	ACATTGCTGA	TCTGAAGATG	GCTGTCAATT	TCAGTCAATT	CAACAGAAGA	TTCTTAAATG	TTGTGCGGCA	GTTTTAGAG	AATGCAGGGA
3701	TACACACAGC	AATATCATTTG	GACCTAATGA	CTGATGCTGA	GCTGGCAGAG	GCTGTATCAT	ACATGCCAAC	ATCTGCAGGA	CAGATAAAAC	TAATGTTAGA

Fig. 39A

HMPV strain 75 (continued)

3801 GAACCGTGCA ATGGTGAGGA GAAAAGGATT TGGAACTCTG ATAGGGGTCT  
3901 GATACACCTT GTTGGATAAT CAAGGCAGCT CCTCTTTGTT CAGAAAAGA  
4001 ATGCAGGATC CACTGTTTAC TACCCAAATA AAAAGACTG CGAAACAAGA  
4101 ATCAAGAGAA TGCAACATCA ACATATCTAC AACCAACTAC CCATGCAAG  
4201 GCTTTGGTGG CTGCTACAA AGGGGTTAGC TGTTCAATTG GCAGTAATCG  
4301 AGGACGCAGA CACTGTAAACA ATTGACAACA CTGTGTATCA ACTAAGCAAA  
4401 CGATCCAATC AAGTTTCTCG AGGATCAGTT CAATGTTGCG CTTGATCAAG  
4501 ATTCTGAACA GTGCAGAAA AGGAAACACT GGCTTCATTA TTGTAATAAT  
4601 TAATCAAAAA AACAGGAAA CCACAGGGG CACTCCAGA TCGTAATGGT  
4701 CAATATAGTA TGTCTCGTAA AGCTCCATGC AAATATGAAG TACGGGCAA  
4801 CTGATAGGTA TTATTTGTTA ATCTCTGAA TCAGCTTTTA  
4901 AGAAGACAGG ACTCAAGACT TTGTTCTTGG TTCTACTAAT GTGGTTCAAG  
5001 CTACATAACA TAATAAACA GTTACAAGAA ATAGAAGTAA GACAGGCCAG  
5101 TATCTTATAT GGAGATGAGC AAAACTCCTG CATCCCTGAT TAATAACCTA  
5201 TTTATCAGCA GGAACCTGATA ATGACTCTTC ATATGCCCTG CAAGACAGTG  
5301 GGCAGATGAT ATGATATGGA CACACAAAGA ATTAAAAGAG ACACGTCTGT  
5401 ATAGAAATAA TATATGTTAA AGTCTACTTA AGTTAGTAAA AAATAAATAG  
5501 CTTGAGAAAT ATGTAATCAA CTCAAAAAAA TGTAAAAAAA ACATCAGGT  
5601 AGTAACAATT ACTGTCAACT ATACAAAAGT AGAAAATAAT TTGCAGGCAT  
5701 TCAACAACAA TCAGACCCAT TCCTGATCTA AATGCAGTAC AGTACCTGAA  
5801 GTTGAGAAAT ACACACGAAT CAATGCACAA ATATFAAAAT ATATAGTTTC  
5901 AGTTCTATGC GACAAAAAGT CAAAAACCAT GACAGAAAAA CATAGGAAAG  
6001 GAGAAAACTC AGTTTTCAC ATTAATAATCA GAACAAATCA TATCTAGATC  
6101 TCACAACACC CTGCGGTCAAT ATGCAATAT CAATGGTCAA ACCACTGTTG  
6201 ACAAGTGGCC ATGGAAGCAA GAGTGGAGAA CAITTCGGGCA ATAGACATGT  
6301 GCTACACTGA TCCTTATGAG ATCAACAGCA CCAAGTATGG CACTCAACAC  
6401 ACTGTGTCAA CATGCCGCG GTAGAACCAA GCAAGAGAC CCCATGACC  
6501 GACCACAGAG GATTCAACAT CTCTAGCAGC AACCTAGAG GACCATCTAC  
6601 GACGAGCACA CAACACTGCT GAGATCAACC AACAGACAGA CCACCACAAAC  
6701 CTCGAACCCAC AAGCACAGCT GCAACCCAAA CACTCAACAC CACCACCAA  
6801 TGCCACAACCT CAAGCAGCG ATCAACCAAC CCAGGCAGCA GACCCAGCT  
6901 ACATCTTCTC CAAGTAGTTA ACAAACAAAAC TATAAAATAA CCATGAAAAAC  
7001 ATGAATTGTT TGAGCGTATA TACTAATGAA ATAGCATCTG TTTGTGCATC  
7101 CAATAACAA TGGATCGGTT TTGTGAATCC ACTGTCAATG TCTATCTTCC  
7201 GCTCATCCCT TTTGAAAAGA CCTTATCTTA AAAAGATAA CACTGTAAA  
7301 CATGACCAAA ATGAAGATAT CAGATTATAA AGTGGTTGAA CCAATTAAAT  
7401 AAACAATTCT TAACAAGAAG TAAAAACATP AGTCCCTTAA AATTAGTAT  
7501 TTAATTTTAT AGATGTGGAG TTTATACCGG TTTGGGTGAG CAATTGGTTT  
7601 AGTAATAAGA ACTGGTTCAA TTTTATGCAG ATCACTAGGC AAGTTAGTTT  
7701 GTAAGTTTTT TCACATATAA CCAACTGTTA ACATGGAAAG ATGTGATGTT

Fig. 39B



HMPV strain 75 (continued)

7801	AAAAACAAGA	AGGACTAGGA	TTTAGAAGTA	ATCTACAAGG	TATGTTAACT	AATAAATTAT	ATGAAAACGT	TGATTATATG	TTAAGTCTAT	GTAGCAATGA	7900
7901	AGGGTTCTCA	CTAGTGAAG	AGTTCGAAG	CTTTATATATG	AGTGAATTC	TTAAAAATFAC	TGAGCATATGCT	CAATTCAGTA	CTAGGTTTAG	GAATACITTTA	8000
8001	TTAAATGGGT	TGACTGAACA	ATTATCAATG	TTGAAGCTA	AAAAAGATC	TAGAGTTCTT	GGCAGTATAT	TGAAAAACAA	TGATTACCCC	ATGTATGAAG	8100
8101	TAGTACTTAA	ATTATTAGG	GACACTTTGA	AAAGTATAAA	ATTATTATTT	AACAAGAAAT	TAGAAAAATG	TAGCAAACTA	TATTATATAT	TCAGAAATTTT	8200
8201	TGGACACCTT	ATGGTAGATG	AGAGGGAAG	AATGATGCT	GTTAAATTA	ATAATGAGAT	TACAAAAAAT	CTTAAACTGG	AGAGCTTAAC	AGAACTAAGA	8300
8301	GGAGCAATTA	TACTAAGAA	TATAAAGGG	TTTGTAGATA	ATAATAAAG	ATGGCCTAAA	ATTAAAGAAAT	TAAAGTGTCT	CAGTAAAGA	TGGTATTATG	8400
8401	ATTTCRAAG	TAAAAGTTAC	CCTAGCCAA	TTGAGCTAAG	TGTACAGAT	TTTTTAGAAC	TTGCTGCAGT	ACAATCGAA	CAGGAATTTT	CTGTCCCTGA	8500
8501	AAAAACAAT	CTTGAGATGG	TATTAAATGA	TAAAGCAATA	TCTCCACCA	AAAAAGTTAAT	ATGGTCGGTA	TATCCAAAA	ATTATCTACC	TGAAATTTATA	8600
8601	AAAAATCAAT	ATTTAGAAGA	GGTCTTCAAT	GCAAGTGACA	GTCAAAAGAAC	GAGGAGAGCT	TTAGAATTTT	ACTTAAAAAG	TTGCAAAAT	GATCAAAAAG	8700
8701	ACCTCAAAAG	TTATGTAACT	AAACAAGAGT	ATCTAAATGA	CAAAGACAC	ATTGTCTCAT	TAACTGGGAA	AGAAAGAGAA	TTAAGTGTAG	GCAGGATGTT	8800
8801	TGCAATGCAA	CCTGGCRAAC	AAAGACAAAT	ACAGTACTA	CCGAGAGAAC	TTTTTAGCTGA	TAATATTGTA	CCCTTTTTC	CAGAACTTT	AACAAGATTT	8900
8901	GGTAGCTGG	ATCTCCAAAG	AATTATGGAA	ATGAATTCAG	AACCTTCTC	CATTAAAACT	AGGAAGAATG	ATAGTTACAA	CAATTATATT	GCAAGAGCCT	9000
9001	CCATAGTAAC	AGACCTAAGT	AAATTCATC	AAGCCTTTAG	ATATGAAC	ACAGCTATCT	GCGCAGACGT	AGCAGATGAG	TTACATGGCA	CGCAAAAGCTT	9100
9101	ATTTTGTGG	TTACATCTTA	TTGTTCCCAT	GACCACAATG	ATATGTGAT	ACAGACATGC	ACCACAGAA	ACAAAGGGG	AGTATGATAT	AGACAAAAATA	9200
9201	GAAGAGCAA	GTGGGCTATA	CAGATACCAT	ATGGAGGGA	TTGAAGGGTG	GTGTCAGAG	TTATGGACAA	TGGAGCGAT	ATCCTTGTTA	GATGTAGTAT	9300
9301	CTGTTAAGAC	TGTTGTCTAG	ATGACCTCTC	TATTAAACGG	AGACAATCAA	TCAATAGATG	TCAGTAAACC	AGTAAATTTG	TCTGAAGTA	TAGATGAAGT	9400
9401	AAAAAGAGAT	TATAGCTTAG	CAATTAATA	GCTTAAAGAG	ATAAGAGATG	CCTATAAAAA	CATTGGCCAT	AAACTCAAAG	AAGGTGAAC	ATATATATCA	9500
9501	AGAGTCTTC	AATTATTAAG	TAAAGTGAT	CAATCTGAGG	GGGTCTGCA	TCCTACCCCC	ATAAAAAAGA	TATTAAAGGT	AGGTCCCTGG	ATAAATACAA	9600
9601	TACTAGATGA	CATTAAACT	AGTGCAGAT	CAATAGGAG	TCTGTGTCAA	GACTATAGAGT	TCAGAGGAGA	AGATATACATA	GTGACTTGA	TATTAAAGAA	9700
9701	TTTCTGGCTG	TATAACTTAT	ACATGCATGA	CTCAAAACAG	CATCCGTAG	CTGGAAAAA	ACTGTTTAAA	CAATTTGACA	AAACACTAAC	ATCTGTGCAA	9800
9801	AGATTTTGG	AGCTGAAGAA	AGAAAATGAT	GTGTTGACC	TATGGATGAA	TATACCAATG	CAGTTTGGAG	GGGAGACCC	AGTAGTTT	TACAGATCTT	9900
9901	TTTACAGAAG	GACTCCTGAT	TTCTTGACTG	AAGCAATCAG	CCATGTGGAT	TTACTGTTAA	AAAGTTTCAA	CAATATATAA	AATGAGACTA	AGATACGAT	10000
10001	CTTTAAAGCC	TTATTATCTA	TAGAAAAGAA	TGAAGCTGCT	ACATTAACAA	CACATAATGAG	AGACCCCCAG	CGGTAGGAT	CGGAAGACA	AGTAAAGTA	10100
10101	ACAAGTGATA	TAAATAGAAC	AGCAGTTACT	AGCATACTGA	GTCTATCTCC	GAATCAGCTA	TTTTTGTGATA	GTGCTATACA	CTATAGCAGA	AATGAAGAAG	10200
10201	AAGTAGGGAT	CATTGCAGAC	AACATAACAC	CTGTTTATCC	TCACGGATTG	AGAGTGCTCT	ATGAATCACT	ACCTTTTCA	AAGGCTGAAA	AGGTTGTCAA	10300
10301	TATGATATCA	GGTACAAAGT	CTATACTAA	CCTATTGCAG	AGAACATCTG	CTATCAATGG	TGAAGATATT	GATAGAGCAG	TGTCTATGAT	GTTAGAGAAC	10400
10401	TTAGGGTTGT	TATCTAGGAT	ATTGTCAGTA	ATAATTAA	GTATAGAAAT	ACCAATTAA	TCCAATGGCA	GATTGATATG	CTGTCAAAAT	TCTAAGACTT	10500
10501	TGAGAGAAA	ATCATGGAAC	AATATGGAAA	TAGTAGGAGT	GACATCTCCA	AGTATTGTAA	CATGTATGGA	TGTTGTGTAT	CGGACTAGTT	CTCATTTTAA	10600
10601	AGGAATAAT	ATTGAAAAT	TCAGTACTGA	CAAGACCACA	AGAGTCCAGA	GGGGACCAA	AAGCCCTTGG	GTAGGATCAA	GCACTCAA	GAAAAAATTA	10700
10701	GTCTCTGTTT	ATAACAGACA	AATCTTTTCA	AAACAACAAA	AAGAGCAACT	GGAAAGCAATA	GGAAAAATGA	GGTGGTGTGA	TAAAGGAAT	CCAGGGCTAA	10800
10801	GAAGATTGCT	CAATAAGATT	TGCATAGGAA	GTTTAGGTAT	TAGCTATAAA	TGTTGTAAC	CTCTATTACC	AGATTATATG	AGTGTAACT	TCTTACATAG	10900
10901	GTATCTGTT	AGTAGCAGAC	CCATGGAAT	CCCAGCTTCT	GTTCCAGCTT	ATAGGACAA	AAATTACCAC	TTTGACACTA	GTCCAATCAA	CCAAGCATTA	11000
11001	AGTGAGAGGT	TCGGGAACGA	AGACATTAA	CTAGTGTTC	AAAATGCAAT	CAGCTGGGA	ATTAGTATAA	TGAGTGTGT	AGAACAGTTA	ACTGGTAGAA	11100
11101	GCCCAAAACA	ATTAGCTTA	ATCCCCCAAT	TAGAAGAGAT	AGATATTATG	CCCCCTCTG	TATTTCAAGG	AAAAATCAAT	TATAAACTAG	TTGATAAAAT	11200
11201	AACCTCCGAT	CAACACATCT	TCAGTCTCTGA	CAAAATAGAC	ATATTAAAC	TAGGCAAGAT	CTTTATGCTT	ACTATAAAG	GTCAAAAAC	TGATCAGTTG	11300
11301	TTAAATTAAGA	GAGAAACTA	TTTCCATGGA	ATAATTTAA	TTGAATCTTT	ATCTGGACGA	CTTGCATGCC	ATTTGGTGG	AAATATAACA	GACACGTGTC	11400
11401	TAGAAAACAA	TATCTTTAGG	AAAGACTGGG	GTGATGGGT	CATATCAGAT	CATGCCCTCA	TGGATTTCAA	GATATTCTTA	TGTGTATTA	AAACCAAACT	11500
11501	TTTATGTAGT	TGGGGATCCC	AAGGGAAAA	TGTAAGAT	GAAGATATAA	TAGATGAATC	CATGACAAA	TTATTAGAA	TTGACACAC	TTTTTGGAGA	11600
11601	ATGTTACGCA	AAGTCATGTT	TGAATCAAG	GTCAAAAAA	GAATATGTT	ATATGATGTA	AAATCTCTAT	CATTAGTAGG	TTATATAGGA	TTTAAAAACT	11700
11701	GGTTTATAGA	GCAGTTAAGA	GTAGTAGAAT	TGCATGAAGT	ACCCTGGATT	GTCAATGCTG	AAGGGAGCT	AGTTGAAAT	AAACCAATCA	AAATTTATTT	11800

Fig. 39C

HMPV strain 75 (continued)

11801	GCAGTTAATA	GAACAAGTC	TATCTTTAAG	AATAACTGTT	TTGAATTATA	CAGACATGGC	ACATGCTCTT	ACAGGATTA	TTAGGAAGAA	ATTGATGTCT	11900
11901	GATTAATGCAC	TCTTTAATCC	AAGTTTCATCA	CCAAATGTTTA	GTCTAACTCA	AGTTATTGAT	CCTACAACAC	AGCTAGACTA	TTTTCTTAAG	GTAATATTGG	12000
12001	AAAGGTTAAA	AAGTTATGAC	ACCAGTTTCAG	ACTACAACAA	AGGGAAGTTA	ACAAGAAATT	ACATGACATT	ATTACCATGG	CAGCACGTAA	ACAGGTATAA	12100
12101	TTTTGCTCTT	AGTTCAACAG	GATGTAAAT	CAGCTTGAAG	ACATGCATCG	GGAAATTGAT	AAAGGACTTA	AACCTAAGG	TTCTTTACTT	TATTGGAGAA	12200
12201	GGAGCAGGTA	ACTGGATGGC	AAGAACAGCA	TGTGAGTATC	CTGACATAAA	ATTTGTATAT	AGGAGTTTAA	AGGATGATCT	TGATCACCAT	TACCCATTAG	12300
12301	AATATCAAAG	GGTAATAGGT	GATTTAAATA	GAGTAATAGA	TGGTGGTGAA	GGATTATCAA	TGGAGACCA	AGATGCAACT	CAAAAGACTC	ATTGGGACTT	12400
12401	GATACACAGA	ATAAGTAAAG	ATGCTTTATT	GATAACATTG	TGTGATGCAG	AATTCAAAA	CAGAGATGAT	TTCTTTTAAA	TGGTAATCT	TGGAGAAAA	12500
12501	CATGTATTAT	CATGTAGAAT	CTGTACAGCT	TATGGAACAG	ATCTTTACTT	ATTTGCAAG	TATCATGCGA	CGGACTGCAA	TATAAAGTTA	CCATTTTTTG	12600
12601	TAAGGTCTGT	AGCTACTTTT	ATTATGCAAG	AGCAATGAGT	GTCAGGATCA	GAATGTTACA	TACTTTTAA	ATTAGGTGAT	CACAATAATC	TGCCATGTCA	12700
12701	CGGAGAAATA	CAAAATCCCA	AAATGAGAA	AGCAATGAGT	AATGATTTCC	ATGCCCTAAA	AAACTAGAC	AACAAATCAA	TTGAAGCAAA	CTGCAAAATCT	12800
12801	CTTCTATCAG	GATTAAGTAA	TCCAAATGGT	TAAAGAAATA	AGCAAGTACA	AAAGAACTG	TTAAACACTAC	AAAGCAATCA	TTCTTTCCATA	GCAACAGTTG	12900
12901	GCGGAAGTAA	GATTATAGAA	TCCAAATGGT	TAAAGAAATA	AGCAAGTACA	ATAATTTGATT	GGTTAGAGCA	TATCTTGAAT	TCTCCAAGAG	GTGAATTTAA	13000
13001	CTATGATTTT	TTTGAAGCAT	TAGAGAACAC	ATATCCCAAT	ATGATCAAGC	TTATAGATAA	CCTGGGAAAT	GCAGAGATAA	AAAAACTAAT	CAAAAGTTACC	13100
13101	GGGTATATGC	TTGTGAGTGA	GAAGTAAATA	TAAATAATA	AATCAACCAT	AATCTCACAC	AATGAGAAA	ATGATCATCT	AACAGTTTAA	TTGACCAATTA	13200
13201	GTAAATTAAA	AATTATAAAT	TAGTAACATA	TTGATAAAAA	ATAAGAAATT	GAAATTGAAT	GTATACGGTT	TTTTTGCCCGT			13280
	10	20	30	40	50		60	70	80	90	100

Fig. 39D